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OM protein - protein search, using sw model
 Run on: April 12, 2005, 15:05:22 ; Search time 31.7965 Seconds
 (without alignments)
 579.883 Million cell updates/sec

Title: US-09-905-247A-8
 Perfect score: 1221 1 DVSFRLSGATSSSKVIFVN. VDAGQVTVSNIALLINRNNA 247
 Sequence: GapOp62
 Scoring table: GapOp 10.0 , Gapext 0.5
 Searched: 513545 seqs, 7449064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backFiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1221	100.0	267	1 US-08-378-761A-74
2	1221	100.0	267	1 US-08-378-761A-74
3	1212	99.3	289	1 US-07-923-692C-4
4	1212	99.3	289	1 US-08-184-237-4
5	1212	99.3	289	2 US-08-82-920-4
6	1212	99.3	289	3 US-08-484-341-4
7	1212	99.3	289	3 US-08-483-502-4
8	1212	99.3	289	4 US-08-726-651A-4
9	1209	99.0	247	1 US-08-488-113B-6
10	1209	99.0	247	1 US-08-477-484B-6
11	1209	99.0	247	2 US-08-646-360-6
12	1209	99.0	247	3 US-08-839-765-6
13	1209	99.0	247	3 US-09-138-389-6
14	1209	99.0	247	3 US-09-510-838-6
15	1209	99.0	247	4 US-09-711-485-6
16	1137	93.1	255	1 US-07-901-707-6
17	1137	93.1	255	1 US-08-425-336-6
18	1137	93.1	255	5 PCT-US92-09487-6
19	1137	93.1	255	5 PCT-US92-09487-6
20	1071	87.7	290	1 US-08-902-486-7
21	1071	87.7	290	1 US-08-245-754A-2
22	1071	87.7	290	2 US-08-597-731-2
23	1071	87.7	495	3 US-08-024-486-15
24	802	65.7	263	1 US-07-901-707-7
25	802	65.7	263	1 US-07-988-430-7
26	802	65.7	263	1 US-08-425-336-7
27	802	65.7	263	1 US-08-488-113B-7

ALIGNMENTS

RESULT 1
 US-08-378-761A-74
 Sequence 74, Application US/08378761A
 Patent No. 5635384

GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A
 APPLICANT: MORGAN, ALICE ER
 TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
 TITLE OF INVENTION: USING
 NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADRESSE: ANDREA T. BORUCKI
 STREET: 9330 ZIONSVILLE ROAD
 CITY: INDIANAPOLIS
 STATE: IN
 COUNTRY: US
 ZIP: 46268

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/378,761A
 FILING DATE: 26-JAN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BORUCKI, ANDREA T
 REGISTRATION NUMBER: 33651
 REFERENCE/DOCKET NUMBER: 38272B

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (317) 337-4846
 INFORMATION FOR SEQ ID NO: 74:

SEQUENCE CHARACTERISTICS:
 LENGTH: 267 amino acids
 TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match Best local Similarity 100.0%; Score 1221; DB 1; Length 267;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 DVSFRLSGATSSSKVIFVN. VDAGQVTVSNIALLINRNNA 247
Db	2 DVSFRLSGATSSSKVIFVN. VDAGQVTVSNIALLINRNNA 247

RESULT 2

US-08-485-286-74

; Sequence 74, Application US/08485286

; Patent No. 5646026

; Patent No. 5646026 5646119

; GENERAL INFORMATION:

; APPLICANT: WALSH, TERENCE A

; APPLICANT: HEY, TIMOTHY D

; APPLICANT: MORGAN, ALICE ER

; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF TITLE OF INVENTION: USING

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ANDREA T. BORUCKI

; STREET: 9330 ZIONSVILLE ROAD

; CITY: INDIANAPOLIS

; STATE: IN

; COUNTRY: US

; ZIP: 46768

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/485,286

; FILING DATE:

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/379761

; FILING DATE: 26-JAN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: BORUCKI, ANDREA T

; REGISTRATION NUMBER: 33651

; REFERENCE/DOCKET NUMBER: 38272B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (317) 337-4946

; INFORMATION FOR SEQ ID NO: 74:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 267 amino acids

; TYPE: amino acid

; STRANDBIASS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-485-286-74

Query Match 100.0%; Score 1221; DB 1; Length 267; Best Local Similarity 100.0%; Pred. No. 2.6e-119; Matches 247; Conservancy 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SVAIDVNVYIMGYRAGDTSFNEASATEAKVFKDAMRKUTLPGSNGVRLQTAGK 120

Db 62 SVAIDVNVYIMGYRAGDTSFNEASATEAKVFKDAMRKUTLPGSNGVRLQTAGK 121

QY 121 IRENIPGLPALSAITTLFYNNANSAASALMVLQIOTSSEARRYKFTBQQLGKRVDKTFL 180

Db 122 IRENIPGLPALSAITTLFYNNANSAASALMVLQIOTSSEARRYKFTBQQLGKRVDKTFL 181

QY 181 PSLAISLENSWALSKQIQTASTNGQFESPVVLINQNRVITTNDAGVTSNALL 240

Db 182 PSLAISLENSWALSKQIQTASTNGQFESPVVLINQNRVITTNDAGVTSNALL 241

QY 241 LNRRNMA 247

Db 242 LNRRNMA 248

RESULT 3

US-07-923-692C-4

; Sequence 4, Application US/07923692C

; Patent No. 5316931

; GENERAL INFORMATION:

; APPLICANT: Donson, Jon

; APPLICANT: Dawson, William O.

; APPLICANT: Grantham, George L.

; APPLICANT: Turpen, Thomas H.

; APPLICANT: Turpen, Ann Myers

; APPLICANT: Garger, Stephen J.

; APPLICANT: Grill, Laurence K.

; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Limbach & Limbach

; STREET: 2001 Ferry Building

; CITY: San Francisco

; STATE: CAL

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/923,692C

; FILING DATE: 31-JUL-1992

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 600,244

; FILING DATE: 22-OCT-1990

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 641,617

; FILING DATE: 16-JAN-1991

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 310,881

; FILING DATE: 17-FEB-1988

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 160,766

; FILING DATE: 26-FEB-1988

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 160,771

; FILING DATE: 26-FEB-1988

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 347,637

; FILING DATE: 05-MAY-1989

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 363,138

; FILING DATE: 08-JUN-1989

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 219,279

; FILING DATE: 15-JUL-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Halluin, Albert P.

; REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: BIOC-20121
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-433-4150
 TELEFAX: 415-33-8716
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 289 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-923-692C-4

Query Match
 Best Local Similarity 99.3%; Score 1212; DB 1; Length 289;
 Matches 245; Conservative 99.2%; Pred. No. 2.5e-118; 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DVSRFLSGATSSSYGVFTSNLRKALPNERKLYDPLRSILPSQRYALIHLTYADETI 60
 Db 24 DVSRFLSGATSSSYGVFTSNLRKALPNERKLYDPLRSILPSQRYALIHLTYADETI 83
 Qy 61 SVAIDVTNVVIMGTRAGDTSYFFNEASATEAKVFKDAMRKVTPYSGNERYLQIOTAAGK 120
 Db 84 SVAIDVTNVVIMGTRAGDTSYFFNEASATEAKVFKDAMRKVTPYSGNERYLQIOTAAGK 143
 121 RENIPLGIPALDSAITTLYFVNANSAAASALMVLQIOTSEARRYKIEQIGKRVDTFL 180
 144 IRENIPLGIPALDSAITTLYFVNANSAAASALMVLQIOTSEARRYKIEQIGKRVDTFL 203
 Qy 181 PSLATISLENSWALSQKIQIASTINGQFESPVVLINAQNQRVITNDAGVTSNIAL 240
 Db 204 PSLATISLENSWALSQKIQIASTINGQFESPVVLINAQNQRVITNDAGVTSNIAL 263
 Qy 241 LNRMNA 247
 Db 264 LNRMNA 270

RESULT 4
 US-08-184-237-4

Sequence 4, Application US/08184237
 Patent No. 5583367
 GENERAL INFORMATION:
 APPLICANT: Dawson, Jon
 APPLICANT: Dawson, William O.
 APPLICANT: Grantham, George L.
 APPLICANT: Turpen, Thomas H.
 APPLICANT: Turpen, Ann Myers
 APPLICANT: Garger, Stephen J.
 APPLICANT: Grill, Laurence K.
 TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Limbach & Limbach
 STREET: 2001 Ferry Building
 CITY: San Francisco
 STATE: CAL
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/184, 237
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 923, 692
 FILING DATE: 31-JUL-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 600, 244
 FILING DATE: 22-OCT-1990

Query Match
 Best Local Similarity 99.3%; Score 1212; DB 1; Length 289;
 Matches 245; Conservative 99.2%; Pred. No. 2.5e-118; 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DVSRFLSGATSSSYGVFTSNLRKALPNERKLYDPLRSILPSQRYALIHLTYADETI 60
 Db 24 DVSRFLSGATSSSYGVFTSNLRKALPNERKLYDPLRSILPSQRYALIHLTYADETI 83
 Qy 61 SVAIDVTNVVIMGTRAGDTSYFFNEASATEAKVFKDAMRKVTPYSGNERYLQIOTAAGK 120
 Db 84 SVAIDVTNVVIMGTRAGDTSYFFNEASATEAKVFKDAMRKVTPYSGNERYLQIOTAAGK 143
 121 RENIPLGIPALDSAITTLYFVNANSAAASALMVLQIOTSEARRYKIEQIGKRVDTFL 180
 144 IRENIPLGIPALDSAITTLYFVNANSAAASALMVLQIOTSEARRYKIEQIGKRVDTFL 203
 Qy 181 PSLATISLENSWALSQKIQIASTINGQFESPVVLINAQNQRVITNDAGVTSNIAL 240
 Db 204 PSLATISLENSWALSQKIQIASTINGQFESPVVLINAQNQRVITNDAGVTSNIAL 263
 Qy 241 LNRMNA 247
 Db 264 LNRMNA 270

RESULT 5
 US-08-482-920-4

Sequence 4, Application US/08482920
 Patent No. 586685
 GENERAL INFORMATION:
 APPLICANT: Dawson, Jon
 APPLICANT: Dawson, William O.
 APPLICANT: Grantham, George L.
 APPLICANT: Turpen, Thomas H.
 APPLICANT: Turpen, Ann Myers
 APPLICANT: Garger, Stephen J.
 APPLICANT: Grill, Laurence K.

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160, 766
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160, 771
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 347, 637
 FILING DATE: 05-MAY-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 363, 138
 FILING DATE: 08-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 219, 279
 FILING DATE: 15-JUL-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Halluin, Albert P.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: BIOC-20121 USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-433-4150
 TELEFAX: 415-433-8716
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 289 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-184-237-4

TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds^B
 STREET: 115 Avenue of the Americas
 CITY: New York
 STATE: New York
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,920
 FILING DATE: 07-JUNE-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 184,237
 FILING DATE: 19-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 600,244
 FILING DATE: 22-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 641,617
 FILING DATE: 16-JAN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 310,881
 FILING DATE: 17-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160,766
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160,771
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 347,637
 FILING DATE: 05-MAY-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Halluin, Albert P.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 8129-112
 APPLICATION NUMBER: US 219,279
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-3660
 TELEFAX: 415-854-3694
 INFORMATION FOR SEQ ID NO: 4:
 LENGTH: 289 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-482-920-4

Query Match Best Local Similarity 99.3%; Score 1212; DB 2; Length 289; Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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  1 DYSFRLSGATSSSYGVFISNLKALPNERKLDIPLRSQPSQVALIHTNYADETI 60
  24 DYSFRLSGATSSSYGVFISNLKALPNERKLDIPLRSQPSQVALIHTNYADETI 83
  61 SVALDVTIVVYIMYRAGDTSYFVNNEASATEAARYVFKDAMRKVTPSPGNVRLQTAGK 120
  84 SVALDVTIVVYIMYRAGDTSYFVNNEASATEAARYVFKDAMRKVTPSPGNVRLQTAGK 143
  121 IENIPNPLGLPALSATITLFFYNNANSASALAMYLQTSSEARYKFEQQGKRVDTFL 180
  144 IENIPNPLGLPALSATITLFFYNNANSASALAMYLQTSSEARYKFEQQGKRVDTFL 203
  
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RESULT 6 US-08-484-341-4
 Sequence 4, Application US/08484341
 GENERAL INFORMATION:
 APPLICANT: Donsen, Jon
 Dawson, William O.
 Grantham, George L.
 Turpen, Thomas H.
 Turpen, Ann Myers
 Garger, Stephen J.
 Grill, Lawrence K.
 TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Limbach & Limbach
 STREET: 2001 Ferry Building
 CITY: San Francisco
 STATE: CAL
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,341
 FILING DATE: 07-Jun-1995
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/184,237
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 600,244
 FILING DATE: 22-OCT-1990
 APPLICATION NUMBER: US 641,617
 FILING DATE: 16-JAN-1991
 APPLICATION NUMBER: US 310,881
 FILING DATE: 17-FEB-1989
 APPLICATION NUMBER: US 160,766
 FILING DATE: 26-FEB-1988
 APPLICATION NUMBER: US 160,771
 FILING DATE: 26-FEB-1988
 APPLICATION NUMBER: US 347,637
 FILING DATE: 05-MAY-1989
 APPLICATION NUMBER: US 363,138
 FILING DATE: 15-JUL-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Halluin, Albert P.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: BIOG-20121 USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-433-150
 TELEFAX: 415-433-8716
 INFORMATION FOR SEQ ID NO: 4:
 LENGTH: 289 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-08-484-341-4

QY 181 PSLAISLENSWALSKQIQTASTNGQFSPSPVVLINAQNORVITNNDAGVTSNIAL 240
 Db 204 PSLAISLENSWALSKQIQTASTNGQFSPSPVVLINAQNORVITNNDAGVTSNIAL 263

Query Match 99.3%; Score 1212; DB 3; Length 289;
 Best Local Similarity 99.2%; Pred. No. 2.5e-118; Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Prior Application Data: US 347,637
 Application Number: US 363,138
 Filing Date: 08-JUN-1989
 Prior Application Data: US 219,279
 Application Number: US 219,279
 Filing Date: 15-JUL-1988
 Attorney/Agent Information:
 Name: Ihnen, Jeffrey L.
 Registration Number: 28,957
 Reference/Doctet Number: 18604-090574
 Telecommunication Information:
 Telephone: 202-962-9100
 Telefax: 202-962-9100
 Information for SEQ ID NO: 4:
 Sequence Characteristics:
 Length: 289 amino acids
 Type: amino acid
 Topology: linear
 Molecular Type: protein
 US-08-483-502-4

RESULT 7

US-08-483-502-4

Sequence 4, Application US/08483502

Patent No. 628492

GENERAL INFORMATION:

Applicant: Danson, Jon

Applicant: Dawson, William O.

Applicant: Grantham, George L.

Applicant: Turpen, Thomas H.

Applicant: Turpen, Ann Myers

Applicant: Garger, Stephen J.

Applicant: Grill, Laurence K.

Title of Invention: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS

Number of Sequences: 11

Correspondence Address:

Addressee: Verable, Baetjer, Howard & Civiletti

Street: 1201 New York Avenue N.W., Suite 1000

City: Washington

State: DC

Country: USA

ZIP: 20005

Computer Readable Form:

Medium Type: Floppy disk

Computer: IBM PC compatible

Operating System: PC-DOS/MS-DOS

Software: Patent In Release #1.0, Version. #1.25

Current Application Data:

Application Number: US/08/483,502

Filing Date:

Classification:

Prior Application Data:

Application Number: 07/739,143

Filing Date:

Application Number: US 600,244

Filing Date: 22-OCT-1990

Prior Application Data:

Application Number: US 641,617

Filing Date: 16-JAN-1991

Prior Application Data:

Application Number: US 310,881

Filing Date: 17-FEB-1989

Prior Application Data:

Application Number: US 160,766

Filing Date: 26-FEB-1988

Prior Application Data:

Application Number: US 160,771

Filing Date: 26-FEB-1988

Prior Application Data:

Application Number: 07/641,617

Query Match 99.3%; Score 1212; DB 3; Length 289;
 Best Local Similarity 99.2%; Pred. No. 2.5e-118; Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Prior Application Data: US 347,637
 Application Number: US 363,138
 Filing Date: 08-JUN-1989
 Prior Application Data: US 219,279
 Application Number: US 219,279
 Filing Date: 15-JUL-1988
 Attorney/Agent Information:
 Name: Ihnen, Jeffrey L.
 Registration Number: 28,957
 Reference/Doctet Number: 18604-090574
 Telecommunication Information:
 Telephone: 202-962-9100
 Telefax: 202-962-9100
 Information for SEQ ID NO: 4:
 Sequence Characteristics:
 Length: 289 amino acids
 Type: amino acid
 Topology: linear
 Molecular Type: protein
 US-08-483-502-4

RESULT 8

US-09-726-651A-4

Sequence 4, Application US/09726651A

Patent No. 648046

GENERAL INFORMATION:

Applicant: Danson, Jon

Applicant: Dawson, William O.

Applicant: Grantham, George L.

Applicant: Turpen, Thomas H.

Applicant: Turpen, Ann M.

Applicant: Garger, Stephen J.

Applicant: Grill, Laurence K.

Title of Invention: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS

File Reference: 008010023CNUS01

Current Application Number: US/09/726,651A

Current Filing Date: 2002-05-02

Prior Application Number: 08/483,502

Prior Filing Date: 1995-06-07

Prior Application Number: 08/184,237

Prior Filing Date: 1994-01-19

Prior Application Number: 07/923,692

Prior Filing Date: 1992-07-31

Prior Application Number: 07/600,244

Prior Filing Date: 1990-10-22

Prior Application Number: 07/641,617

PRIOR FILING DATE: 1991-01-15
 PRIOR APPLICATION NUMBER: 07/737,899
 PRIOR FILING DATE: 1991-07-26
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 4
 LENGTH: 289
 TYPE: PRT
 ORGANISM: Chinese Cucumber alpha-trichosanthin
 US-09-726-651A-4

Query Match 99.3%; Score 1212; DB 4; Length 289;
 Best Local Similarity 99.2%; Pred. No. 2.5e-18; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSFRLSGATSSSYGVFISNRKALPNERKLYDPLRSLPGSQRVALIHLTNYADETI 60
 Db 24 DVSFRLSGATSSSYGVFISNRKALPNERKLYDPLRSLPGSQRVALIHLTNYADETI 83

Qy 61 SVAVDVTNVVYNGYRAGDTSYFFNEASATEAKVFKDAMRKVTLPGSGNVERLQTAGK 120
 Db 84 SVAVDVTNVVYNGYRAGDTSYFFNEASATEAKVFKDAMRKVTLPGSGNVERLQTAGK 143

Qy 121 IRENIPGLPGLDSDAITLETLYNANSASALMVLQIOTSEARRYKFEQQIGKRVDTFL 180
 Db 144 IRENIPGLPGLDSDAITLETLYNANSASALMVLQIOTSEARRYKFEQQIGKRVDTFL 203

Qy 181 PSIAITISLENSWALSALKOIQIASTNINGQFESPVVLINAQNORVITTNDAGVTSNALL 240
 Db 204 PSIAITISLENSWALSALKOIQIASTNINGQFESPVVLINAQNORVITTNDAGVTSNALL 263

Qy 241 LNRNNMA 247
 Db 264 LNRNNMA 270

RESULT 9
 US-08-488-113B-6
 Sequence 6, Application US/08488113B
 Patent No. 5,74580
 GENERAL INFORMATION:
 APPLICANT: Bettier, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnika, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,113B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/425,336
 FILING DATE: 18-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:

Query Match 99.0%; Score 1209; DB 1; Length 247;
 Best Local Similarity 99.2%; Pred. No. 4.1e-18; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSFRLSGATSSSYGVFISNRKALPNERKLYDPLRSLPGSQRVALIHLTNYADETI 60
 Db 1 DVSFRLSGATSSSYGVFISNRKALPNERKLYDPLRSLPGSQRVALIHLTNYADETI 60

Qy 61 SVAVDVTNVVYNGYRAGDTSYFFNEASATEAKVFKDAMRKVTLPGSGNVERLQTAGK 120
 Db 61 SVAVDVTNVVYNGYRAGDTSYFFNEASATEAKVFKDAMRKVTLPGSGNVERLQTAGK 120

Qy 121 IRENIPGLPGLDSDAITLETLYNANSASALMVLQIOTSEARRYKFEQQIGKRVDTFL 180
 Db 121 IRENIPGLPGLDSDAITLETLYNANSASALMVLQIOTSEARRYKFEQQIGKRVDTFL 180

Qy 181 PSIAITISLENSWALSALKOIQIASTNINGQFESPVVLINAQNORVITTNDAGVTSNALL 240
 Db 181 PSIAITISLENSWALSALKOIQIASTNINGQFESPVVLINAQNORVITTNDAGVTSNALL 240

Qy 241 LNRNNMA 247
 Db 241 LNRNNMA 247

RESULT 10
 US-08-477-484B-6
 Sequence 6, Application US/08477484B
 Patent No. 5,756699
 GENERAL INFORMATION:
 APPLICANT: Bettier, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnika, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,484B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/425,336
 FILING DATE: 18-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155

US-08-488-113B-6
 TELIX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 247 amino acids
 TYPE: amino acid
 TOPOGY: linear
 MOLECULE TYPE: protein

US-08-477-484B-6
 TELIX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 247 amino acids
 TYPE: amino acid
 TOPOGY: linear
 MOLECULE TYPE: protein

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/425,336
 FILING DATE: 18-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 247 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-477-184B-5

Query Match 99.0%; Score 1209; DB 1;
 Best Local Similarity 99.2%; Pred. No. 4.1e-18;
 Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 Db 1 DVSPRLSGATSSSYGVFTSNRKALPNERKLYDPLRSLSLPGSQRVALIHLTNYADBTI 60
 Qy 61 SVAIDVNTVNYIMGYRAGDTSYFNEASATEAKVFKDMRKVTLPSGNYERLQTAGK 120
 Db 61 SVAIDVNTVNYIMGYRAGDTSYFNEASATEAKVFKDMRKVTLPSGNYERLQTAGK 120
 Qy 121 IRENIPGLPGLPADSATTLYFVNANSASALMVLQISTSEARRYKFIEQOIGRKVDPFL 180
 Db 121 IRENIPGLPGLPADSATTLYFVNANSASALMVLQISTSEARRYKFIEQOIGRKVDPFL 180
 Qy 181 PSIAIISLENSWMSLSKQIOLASTNNGQFESPVVLINAQNQRTITNDAGVTSNALL 240
 Db 181 PSIAIISLENSWMSLSKQIOLASTNNGQFESPVVLINAQNQRTITNDAGVTSNALL 240
 Qy 241 LNRRNMA 247
 Db 241 LNRRNMA 247

RESULT 11
 US-08-646-360-6
 Sequence 6, Application US/08646360
 Patent No. 583491
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnica, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA

ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 247 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-646-360-6

Query Match 99.0%; Score 1209; DB 2;
 Best Local Similarity 99.2%; Pred. No. 4.1e-18;
 Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 Db 1 DVSPRLSGATSSSYGVFTSNRKALPNERKLYDPLRSLSLPGSQRVALIHLTNYADBTI 60
 Qy 61 SVAIDVNTVNYIMGYRAGDTSYFNEASATEAKVFKDMRKVTLPSGNYERLQTAGK 120
 Db 61 SVAIDVNTVNYIMGYRAGDTSYFNEASATEAKVFKDMRKVTLPSGNYERLQTAGK 120
 Qy 121 IRENIPGLPGLPADSATTLYFVNANSASALMVLQISTSEARRYKFIEQOIGRKVDPFL 180
 Db 121 IRENIPGLPGLPADSATTLYFVNANSASALMVLQISTSEARRYKFIEQOIGRKVDPFL 180
 Qy 181 PSIAIISLENSWMSLSKQIOLASTNNGQFESPVVLINAQNQRTITNDAGVTSNALL 240
 Db 181 PSIAIISLENSWMSLSKQIOLASTNNGQFESPVVLINAQNQRTITNDAGVTSNALL 240
 Qy 241 LNRRNMA 247
 Db 241 LNRRNMA 247

RESULT 12
 US-08-839-765-6
 Sequence 6, Application US/08839765
 Patent No. 6146631
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 NUMBER OF SEQUENCES: 169
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/839,765
 FILING DATE: 15-APR-1997
 CLASSIFICATION: 520
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/425,336
 FILING DATE: 18-APR-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/054,691
 FILING DATE: 12-MAY-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 247 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-0-839-765-6

Query Match 99.0%; Score 1209; DB 3; Length 247;
 Best Local Similarity 99.2%; Pred. No. 4.1e-18; Mismatches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DVSPRLSGATSSYGVFISNRKALPNERKLYDIPRLSSLPGSQRVALIHLNTYADETI 60
 Db 1 DVSPRLSGATSSYGVFISNRKALPNERKLYDIPRLSSLPGSQRVALIHLNTYADETI 60

Qy 61 SVAIDVNVVYNGRAGDTSYFVNEASATEAAKYVKFDAMRKVTLPYSGNVERLQTAAGK 120
 Db 61 SVAIDVNVVYNGRAGDTSYFVNEASATEAAKYVKFDAMRKVTLPYSGNVERLQTAAGK 120

Qy 121 IRBNPIPLGLPALSATITLYFTYNSAASALAMVLIQSTSEAAKYKPEQQIGRKVKTFL 180
 Db 121 IRBNPIPLGLPALSATITLYFTYNSAASALAMVLIQSTSEAAKYKPEQQIGRKVKTFL 180

Qy 181 PSLAITSLENSMSALSKOIQIASTNNQFESPVVLINAQNQRTITNDAGVTSNIAL 240
 Db 181 PSLAITSLENSMSALSKOIQIASTNNQFESPVVLINAQNQVATITNDAGVTSNIAL 240

Qy 241 LARNNMA 247

RESULT 13 ; Sequence 6, Application US/09136389
 ; General Information:
 ; Patent No. 6146850
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; NUMBER OF SEQUENCES: 173
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136,389
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/054,691
 FILING DATE: 12-MAY-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 247 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-0-839-765-6

Query Match 99.0%; Score 1209; DB 3; Length 247;
 Best Local Similarity 99.2%; Pred. No. 4.1e-18; Mismatches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DVSPRLSGATSSYGVFISNRKALPNERKLYDIPRLSSLPGSQRVALIHLNTYADETI 60
 Db 1 DVSPRLSGATSSYGVFISNRKALPNERKLYDIPRLSSLPGSQRVALIHLNTYADETI 60

Qy 61 SVAIDVNVVYNGRAGDTSYFVNEASATEAAKYVKFDAMRKVTLPYSGNVERLQTAAGK 120

Db 61 SVAIDVTVNYIMGYRAGDTSYFFNEASATEAKVVFKDAKVTLPYSGNVRLQTAGK 120 ;
 Qy 121 IRENIPGLPALSATIILFYVANSASALMVLQTSSEARYKFEQQIGRKVDTFL 180 ;
 Db 121 IRENIPGLPALSATIILFYVANSASALMVLQTSSEARYKFEQQIGRKVDTFL 180 ;
 Qy 181 PSAIISIENSWSALSKQIQTQIASTNGQFESPVVLINAQNQRTITNDAGVTSNIAL 240 ;
 Db 181 PSAIISIENSWSALSKQIQTQIASTNGQFESPVVLINAQNQRTITNDAGVTSNIAL 240 ;
 Qy 241 LNRNNMA 247 ;
 Db 241 LNRNNMA 247 ;

RESULT 14 ;
 US-09-610-838-6 Application US/09610838 ;
 Sequence 5, Application US/09610838 ;
 Patent No. 6376217 ;
 GENERAL INFORMATION: ;
 APPLICANT: Better, Marc D. ;
 APPLICANT: Carroll, Stephen F. ;
 APPLICANT: Studnika, Gary M. ;
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins ;
 NUMBER OF SEQUENCES: 173 ;
 CORRESPONDENCE ADDRESS: ;
 ADDRESSEE: McAndrews, Held & Malloy, Ltd. ;
 STREET: 500 West Madison Street, 34th floor ;
 CITY: Chicago ;
 STATE: Illinois ;
 COUNTRY: USA ;
 ZIP: 60661 ;

COMPUTER READABLE FORM: ;
 MEDIUM TYPE: Floppy disk ;
 COMPUTER: IBM PC compatible ;
 OPERATING SYSTEM: PC-DOS/MS-DOS ;
 SOFTWARE: Patent in Release #1.0, Version #1.25 ;
 CURRENT APPLICATION DATA: ;
 APPLICATION NUMBER: US/09/610,838 ;
 FILING DATE: 06-JUL-2000 ;
 CLASSIFICATION: ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US/09/136,389 ;
 FILING DATE: 18-AUG-1998 ;
 APPLICATION NUMBER: 08/646,360 ;
 FILING DATE: 13-MAY-1996 ;
 APPLICATION NUMBER: PCT/US94/05348 ;
 FILING DATE: 12-MAY-1994 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 08/064,691 ;
 FILING DATE: 12-MAY-1993 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 07/988,430 ;
 FILING DATE: 09-DEC-1992 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 07/901,707 ;
 FILING DATE: 19-JUN-1992 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 07/787,567 ;
 FILING DATE: 04-NOV-1991 ;
 ATTORNEY/AGENT INFORMATION: ;
 NAME: McNicholas, Janet M. ;
 REGISTRATION NUMBER: 32,918 ;
 REFERENCE/DOCKET NUMBER: 200-70-24 ;
 TELECOMMUNICATION INFORMATION: ;
 TELEPHONE: 312/707-8889 ;
 TELEFAX: 312/707-9155 ;
 INFORMATION FOR SEQ ID NO: 6: ;
 SEQUENCE CHARACTERISTICS: ;
 LENGTH: 247 amino acids ;
 TYPE: amino acid ;

RESULT 15 ;
 US-09-711-485-6 ;
 Sequence 6, Application US/09711485 ;
 Patent No. 6649742 ;
 GENERAL INFORMATION: ;
 APPLICANT: Better, Marc D. ;
 APPLICANT: Carroll, Stephen F. ;
 APPLICANT: Studnika, Gary M. ;
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins ;
 NUMBER OF SEQUENCES: 169 ;
 CORRESPONDENCE ADDRESS: ;
 ADDRESSEE: McAndrews, Held & Malloy, Ltd. ;
 STREET: 500 West Madison Street, 34th floor ;
 CITY: Chicago ;
 STATE: Illinois ;
 COUNTRY: USA ;
 ZIP: 60661 ;

COMPUTER READABLE FORM: ;
 MEDIUM TYPE: Floppy disk ;
 COMPUTER: IBM PC compatible ;
 OPERATING SYSTEM: PC-DOS/MS-DOS ;
 SOFTWARE: Patent in Release #1.0, Version #1.25 ;
 CURRENT APPLICATION DATA: ;
 APPLICATION NUMBER: US/09/711,485 ;
 FILING DATE: ;
 CLASSIFICATION: ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: 08/839,765 ;
 FILING DATE: ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 08/064,691 ;
 FILING DATE: 12-MAY-1993 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 07/988,430 ;
 FILING DATE: 09-DEC-1992 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 07/901,707 ;
 FILING DATE: 19-JUN-1992 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 07/787,567 ;
 FILING DATE: 04-NOV-1991 ;
 ATTORNEY/AGENT INFORMATION: ;
 NAME: McNicholas, Janet M. ;

; TOPOLGY: linear
 ; MOLECULE TYPE: protein
 US-09-610-838-6
 Query Match Best Local Similarity 99.0%; Score 1209; DB 3; Length 247;
 Matches 245; Conservative 99.2%; Pred. No. 4, 1e-118; Indels 0; Gaps 0;
 Db 121 IRENIPGLPALSATIILFYVANSASALMVLQTSSEARYKFEQQIGRKVDTFL 180 ;
 Qy 1 DVSRFLSGATSSYYGVTSNRKALPVERKUDIPURSSLPGSQRALIHTNADBTI 60 ;
 Db 1 DVSRFLSGATSSYYGVFSNRKALPVERKUDIPURSSLPGSQRALIHTNADBTI 60 ;
 Db 61 SVAIDVTVNYIMGYRAGDTSYFFNEASATEAKVVFKDAKVTLPYSGNVRLQTAGK 120 ;
 Qy 181 PSAIISIENSWSALSKQIQTQIASTNGQFESPVVLINAQNQRTITNDAGVTSNIAL 240 ;
 Db 181 PSAIISIENSWSALSKQIQTQIASTNGQFESPVVLINAQNQRTITNDAGVTSNIAL 240 ;
 Qy 241 LNRNNMA 247 ;
 Db 241 LNRNNMA 247 ;

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; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-711-485-6

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Query Match      99.0%;  Score 1209;  DB 4;  Length 247;
Best Local Similarity 99.2%;  Pred. No. 4.1e-18;  Matches 245;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;
Matches 245;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;
Qy      1 DYSFRLLSGATSSSYGVFTSNLRKALPWERKVDIPLRSLSGSQRVALHILTYADETI 60
Db      1 DYSFRLLSGATSSSYGVFTSNLRKALPWERKVDIPLRSLSGSQRVALHILTYADETI 60
Qy      61 SVAIDVTVVYIMYRAGDTSYFFNEASATEAAKVVFQDAMRKVTLPSGNVERLQTAGK 120
Db      61 SVAIDVTVVYIMYRAGDTSYFFNEASATEAAKVVFQDAMRKVTLPSGNVERLQTAGK 120
Qy      121 IRENIPGLPALSAITLFLYNNANSASALMVLIOSTSEAAKYKFLBQQIGKRVDKTFL 180
Db      121 IRENIPGLPALSAITLFLYNNANSASALMVLIOSTSEAAKYKFLBQQIGKRVDKTFL 180
Qy      181 PSLAITSLENSMALSQKIQIASTNNQFESPVLINAQNORTITNDAGVTSNALL 240
Db      181 PSLAITSLENSMALSQKIQIASTNNQFESPVLINAQNORTITNDAGVTSNALL 240
Qy      241 LNRRNMA 247
Db      241 LNRRNMA 247

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Search completed: April 12, 2005, 15:16:15
 Job time : 32.7366 Secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: April 12, 2005, 14:53:56 ; Search time 111.519 Seconds
(without alignments) 856.626 Million cell updates/sec

Title: US-09-905-247A-8
Perfect score: 1221
Sequence: 1 DVSFRRLSGATSSSYGVFISN. VDAGSVNTSNIAALLNRRNMA. 247

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqD19808:*

2: geneseqD19908:*

3: geneseqD20008:*

4: geneseqD20018:*

5: geneseqD20028:*

6: geneseqD20038:*

7: geneseqD2003b8:*

8: geneseqD20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

RESULT 1					
ID	AY69048	AY69048 standard, protein; 247 AA.			
XX					
AC	AY69048;				
XX					
DT	06-AUG-2003	(revised)			
XX	30-MAY-2000	(first entry)			
DE	Amino acid sequence of exemplary cell toxin trichosanthin.				
XX	Chemokine receptor; ligand; inflammatory response; immune effector cell; secondary tissue damage; central nervous system injury; trichosanthin; CNS inflammatory disease; neurodegenerative disorder; heart disease; inflammatory eye disease; inflammatory bowel disease; PCR primer; inflammatory joint disease; inflammatory kidney; renal disease; inflammatory lung disease; inflammatory nasal disease; thyroditis; inflammatory thyroid disease; cytokine-regulated cancer; ss.				
XX	inflammatory disease; inflammatory eye disease; inflammatory bowel disease; PCR primer; inflammatory joint disease; inflammatory kidney; renal disease; inflammatory lung disease; inflammatory nasal disease; thyroditis; inflammatory thyroid disease; cytokine-regulated cancer; ss.				
OS	Trichosanthes kirilowii.				
XX	Trichosanthes kirilowii.				
PN	W0200004926-A2.				
XX					
PD	03-FEB-2000.				
XX					
PR	21-JUL-1999;	99WO-CA000559.			
XX					
PR	22-JUL-1998;	98US-0012023.			
XX					
PA	(OSPR-) OSPREY PHARM LTD.				
XX	(OSPR-) OSPREY PHARM LTD.				
PI	McDonald JR, Coggins PJ;				
XX	McDonald JR, Coggins PJ;				
DR	WPI; 2000-182542/16.				
XX	WPI; 2000-182542/16.				
PS	Disclosure; Page 67; 204pp; English.				
XX	The present sequence represents an exemplary cell toxin, which can be incorporated into the conjugates of the invention. The specification describes a conjugate, comprising a targeted agent and a chemokine receptor ligand. The conjugate binds to a chemokine receptor resulting in internalisation of the targeted agent in cells bearing the receptor. The conjugates are used for formulating a medicament or for treating disorders associated with inflammatory responses resulting from				

Aar37295 Plant typ
Aar63907 Type I ri
Aar69043 Amino aci
Aab36824 Residues
Aab1299 Wild type
Aab105683 Bryonia d
Aar74182 Type I ri
Aar37296 Plant typ
Aaw21707 Monordin.
Aaw25144 Monordin
Aar29909 Prod. of
Aar07522 Alpha-Tri
Aar25572 Ribosome
Aar29910 Prod. of
Aar07521 Alpha-Tri

Aar37295 Plant typ
Aar63907 Type I ri
Aar69043 Amino aci
Aab36824 Residues
Aab1299 Wild type
Aab105683 Bryonia d
Aar74182 Brydin 1
Aab36828 BD-G28.5
Aab01300 Altered b
Aoi05689 Bryonia d
Aar63908 Type I ri
Aar74182 Type I ri
Aar37296 Plant typ
Aaw21707 Monordin.
Aaw25144 Monordin
Aar29909 Prod. of
Aar07522 Alpha-Tri
Aar25572 Ribosome
Aar29910 Prod. of
Aar07521 Alpha-Tri

Aar37295 Plant typ
Aar63907 Type I ri
Aar69043 Amino aci
Aab36824 Residues
Aab1299 Wild type
Aab105683 Bryonia d
Aar74182 Brydin 1
Aab36828 BD-G28.5
Aab01300 Altered b
Aoi05689 Bryonia d
Aar63908 Type I ri
Aar74182 Type I ri
Aar37296 Plant typ
Aaw21707 Monordin.
Aaw25144 Monordin
Aar29909 Prod. of
Aar07522 Alpha-Tri
Aar25572 Ribosome
Aar29910 Prod. of
Aar07521 Alpha-Tri

26	1137	93.1	255	2	AAR37295
27	1137	93.1	255	2	AAR63907
28	1071	87.7	247	4	Aar69043
29	1071	87.7	248	4	AAB36824
30	1071	87.7	267	3	AAB01299
31	1071	87.7	267	8	ADT05683
32	1071	87.7	290	2	AAR92481
33	1071	87.7	496	4	AAB36828
34	1044	85.5	367	3	AAB01300
35	886	72.6	267	8	ADT05689
36	802	65.7	263	2	AAR63908
37	802	65.7	263	2	AAR74182
38	795	65.1	263	2	AAR37295
39	762	62.4	250	2	AAW21707
40	762	62.4	250	2	AAW25144
41	754	61.8	277	2	AAR29909
42	740	60.5	272	2	AAR07522
43	740	60.5	272	2	AAR29910
44	728.5	59.7	278	2	AAR07521
45	728.5	59.7	280	2	AAR07521

ALIGNMENTS

26	1137	93.1	255	2	AAR37295
27	1137	93.1	255	2	AAR63907
28	1071	87.7	247	4	Aar69043
29	1071	87.7	248	4	AAB36824
30	1071	87.7	267	3	AAB01299
31	1071	87.7	267	8	ADT05683
32	1071	87.7	290	2	AAR92481
33	1071	87.7	496	4	AAB36828
34	1044	85.5	367	3	AAB01300
35	886	72.6	267	8	ADT05689
36	802	65.7	263	2	AAR63908
37	802	65.7	263	2	AAR74182
38	795	65.1	263	2	AAR37295
39	762	62.4	250	2	AAW21707
40	762	62.4	250	2	AAW25144
41	754	61.8	277	2	AAR29909
42	740	60.5	272	2	AAR07522
43	740	60.5	272	2	AAR29910
44	728.5	59.7	278	2	AAR07521
45	728.5	59.7	280	2	AAR07521

26	1137	93.1	255	2	AAR37295
27	1137	93.1	255	2	AAR63907
28	1071	87.7	247	4	Aar69043
29	1071	87.7	248	4	AAB36824
30	1071	87.7	267	3	AAB01299
31	1071	87.7	267	8	ADT05683
32	1071	87.7	290	2	AAR92481
33	1071	87.7	496	4	AAB36828
34	1044	85.5	367	3	AAB01300
35	886	72.6	267	8	ADT05689
36	802	65.7	263	2	AAR63908
37	802	65.7	263	2	AAR74182
38	795	65.1	263	2	AAR37295
39	762	62.4	250	2	AAW21707
40	762	62.4	250	2	AAW25144
41	754	61.8	277	2	AAR29909
42	740	60.5	272	2	AAR07522
43	740	60.5	272	2	AAR29910
44	728.5	59.7	278	2	AAR07521
45	728.5	59.7	280	2	AAR07521

CC activation, proliferation and migration of immune effector cells. The
 CC disorders or disease states comprise secondary tissue damage such as
 CC central nervous system (CNS) injury, CNS inflammatory diseases,
 CC neurodegenerative disorders, heart disease, inflammatory eye diseases,
 CC inflammatory bowel diseases, inflammatory joint diseases, inflammatory
 CC kidney or renal diseases, inflammatory lung diseases, inflammatory nasal
 CC diseases, inflammatory thyroid disease such as thyroiditis, or cytokine-
 XX regulated cancers. (Updated on 06-AUG-2003 to correct OS field.)
 SQ Sequence 247 AA;

Query Match 100.0%; Score 1221; DB 3; Length 247;
 Best Local Similarity 100.0%; Pred. No. 9e-111; Mismatches 0; Indels 0; Gaps 0;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSFRLSGATSSSYGVFISNRKALPNERKLYDIPRLSSLPGSQRVALHTLNAYDETI 60
 Db 1 DVSFRLSGATSSSYGVFISNRKALPNERKLYDIPRLSSLPGSQRVALHTLNAYDETI 60
 Db 1 DVSFRLSGATSSSYGVFISNRKALPNERKLYDIPRLSSLPGSQRVALHTLNAYDETI 60
 Qy 61 SVAIDTVNIVYNGYRAGDTSYFNEASATEAKVYFKDAMKRVTLPSGNVERQTAGK 120
 Db 61 SVAIDTVNIVYNGYRAGDTSYFNEASATEAKVYFKDAMKRVTLPSGNVERQTAGK 120
 Qy 121 IRENPIGLPALSATTLFVYNNANSASALAMVLQTSSEARRYKTEQQIGRKVDTFL 180
 Db 121 IRENPIGLPALSATTLFVYNNANSASALAMVLQTSSEARRYKTEQQIGRKVDTFL 180
 Qy 181 PSLAISLENSWALSQIQIASTNGQFESPVVLINAQNQRTITNDAGVVSNIALL 240
 Db 181 PSLAISLENSWALSQIQIASTNGQFESPVVLINAQNQRTITNDAGVVSNIALL 240
 Qy 241 LNRNNMA 247
 Db 241 LNRNNMA 247

RESULT 2

AAR07518 ID AAR07518 standard; protein; 248 AA.
 XX AC AAR07518;
 XX DT 06-FEB-1991 (first entry)
 DE Synthetic alpha-trichosanthin.
 KW trichosanthin (TCS); Human Immunodeficiency Virus; inhibition.
 OS Trichosanthes kirilowii.
 XX PN WO9012097-A.
 XX PD 18-OCT-1990.
 XX PP 04-APR-1989; 89US-00333184.
 XX PR 04-APR-1989; 89US-00333184.
 XX PA (GENE-) GENELABS INC.
 XX PI Piatek M, Chow T, Fry K;
 XX DR WPI; 1990-334847/44.
 XX N-PSDB; AAQ06346.

PT Recombinant trichosanthin protein - with selective inhibitory effect on
 viral expression in HIV infected T-cells or monocyte-macrophage.
 XX Example; Fig 11; 102pp; English.

CC Encoded by a synthetic gene containing unique restriction sites spaced 20
 to 90 bp apart. Introduction of mutations is facilitated by cassette
 replacement. The effect of mutations on inhibitory action can be

CC investigated. For example, a double mutant containing the amino acid
 CC substitutions Glu(160) to Asp and Arg(163) to Lys was found to be almost
 CC 3 times less active at inhibiting in vitro translation in rabbit
 CC reticulocyte lysate. See also AAQ06343-5 and AAQ06347-Q06351
 XX SQ Sequence 248 AA;

Query Match 100.0%; Score 1221; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 9.1e-111; Mismatches 0; Indels 0; Gaps 0;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSFRLSGATSSSYGVFISNRKALPNERKLYDIPRLSSLPGSQRVALHTLNAYDETI 61
 Db 2 DVSFRLSGATSSSYGVFISNRKALPNERKLYDIPRLSSLPGSQRVALHTLNAYDETI 61
 Db 62 SVAIDTVNIVYNGYRAGDTSYFNEASATEAKVYFKDAMKRVTLPSGNVERQTAGK 121
 Qy 121 IRENPIGLPALSATTLFVYNNANSASALAMVLQTSSEARRYKTEQQIGRKVDTFL 180
 Db 122 IRENPIGLPALSATTLFVYNNANSASALAMVLQTSSEARRYKTEQQIGRKVDTFL 181
 Qy 181 PSLAISLENSWALSQIQIASTNGQFESPVVLINAQNQRTITNDAGVVSNIALL 240
 Db 182 PSLAISLENSWALSQIQIASTNGQFESPVVLINAQNQRTITNDAGVVSNIALL 241
 Qy 241 LNRNNMA 247
 Db 242 LNRNNMA 248

RESULT 3

AAR25573 ID AAR25573 standard; protein; 248 AA.
 XX AC AAR25573;
 XX DT 25-MAR-2003 (revised)
 DT 13-JAN-1993 (first entry)
 XX DE Mature alpha-trichosanthin.
 XX TCS; alpha-trichosanthin; Radix trichosanthin; abortifacient;
 KW ribosome inactivating protein; RIP; HIV-infected human T cells;
 KW human immunodeficiency virus; Trichosanthes kirilowii; ss.
 OS Synthetic.
 XX US5128460-A.
 XX PR 04-APR-1990; 90US-00504775.
 XX PR 04-APR-1989; 89US-00333184.
 XX PR 07-SEP-1989; 89US-00404326.
 XX PA (GENE-) GENELABS INC.
 XX PI Piatek M, Chow TP, Fry K;
 XX DR WPI; 1992-249485/30.
 XX N-PSDB; AAQ25573.

PT Nucleic acid encoding trichosanthin protein - which can be used to
 PT inactivate ribosome(s) to inhibit protein synthesis or to inhibit HIV
 PT expression.
 XX Example 6; Fig 11; 53pp; English.

CC A synthetic alpha-trichosanthin gene was constructed to facilitate
 CC mutational analysis of alpha-TCS in experiments to investigate structure-

CC function relationships. The synthetic gene contains unique restriction sites spaced 20-90bp apart. The translation product of the synthetic gene corresponds to the mature alpha TCS. Variants of the protein can be generated by mutagenesis of the synthetic gene. The variants can then be screened for changes in ribosome inhibitory and/or HIV-1 inhibitory activities. See AAQ2699-Q26503. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR field.)

CC SQ Sequence 248 AA;

Query Match 100.0%; Score 1221; DB 2; Length 248; Best Local Similarity 100.0%; Pred. No. 9, 1e-111; Mismatches 0; Indels 0; Gaps 0; Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFRLCGATSSYGVFISNLKALPNEKLYVPLRSLSPOSQVALIHTNYADETI 60

DB 2 DVSFRLCGATSSYGVFISNLKALPNEKLYVPLRSLSPOSQVALIHTNYADETI 61

QY 61 SVAIDVTNVYIMGRAGDTSYFNEASATEAKVVFKAQKVTLPYSGNYERLQTAGK 120

DB 62 SVAIDVTNVYIMGRAGDTSYFNEASATEAKVVFKAQKVTLPYSGNYERLQTAGK 121

QY 121 IRENIPIGLPLADSATITLYFVNANSASALMVLQISTSEARVKEFQOIGKRVDTPL 180

DB 122 IRENIPIGLPLADSATITLYFVNANSASALMVLQISTSEARVKEFQOIGKRVDTPL 181

QY 181 PSIAIISLENSWALSKOIQIOLASTNNGQFESPVVLINAQNQRTITINVDAGVTSNALL 240

DB 182 PSIAIISLENSWALSKOIQIOLASTNNGQFESPVVLINAQNQRTITINVDAGVTSNALL 241

QY 241 LNRNNMA 247

DB 242 LNRNNMA 248

RESULT 4

AAW21703

ID AAW21703 standard; protein; 267 AA.

XX

AC AAW21703;

XX

DT 25-MAR-2003 (revised)

DT 26-SEP-1997 (first entry)

DE

XX

Trichosanthin.

XX

KW pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer; inactivation; eukaryotic ribosome; alpha fragment; beta fragment; inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.

OS Trichosanthes kirilowii.

XX

FH

FT

XX

PN US5635384-A.

FH

Key Region

13.9 - 149

/note="Position of possible insertion of internal peptide linker sequence"

RESULT 5

AAW25140

ID AAW25140 standard; protein; 267 AA.

XX

AC AAW25140;

XX

DT 25-MAR-2003 (revised)

DT 02-DEC-1997 (first entry)

XX

DE Trichosanthin (a ribosome inhibitory protein) inactive precursor.

XX

Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;

XX Internal linker; Barley translation Inhibitor; Trichosanthin;

XX Ricin A-chain; Abrin-A A-chain; Saporin; SIT-1; Luffin A; MAP;

XX Ricinus communis agglutinin; Monodend; PAP-S; Luffin-B; Dianthin 30;

XX therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;

XX post-translational modification; cancer; neoplasia; HIV; AIDS;

XX human immunodeficiency virus; acquired immune deficiency syndrome.

XX OS Synthetic.

XX US5646026-A.

XX PN

PD 08-JUL-1997.

XX

DE Hey TD, Morgan AER, Walsh TA;

XX DR

XX WPI; 1997-399831/28.

PT Inactive precursor of maize ribosome-inactivating protein - also chimeric ribosome-inactivating protein precursors containing internal linker sequences.

PT

XX

CC

XX Native trichosanthin (TCS) protein sequence.

DE XX

XX Trichosanthin; TCS; mutant; MTCS; therapeutic; cytostatic; antitumour;

KW anti-human immunodeficiency virus; virucide; immunostimulant; gene;

KW ectopic pregnancy.

XX OS Trichosanthes kirilowii.

PH FT

Key Peptide Location/Qualifiers

1. .23 /note= "signal peptide"

Misc-difference 6 /note= "encoded by GAC"

FT Protein 24. .289 /note= "mature protein"

FT Region 174. .180 /note= "MTCS contains a modification of at least one amino acid residue in this region"

FT Misc-difference 175 /note= "encoded by ATT"

FT Region 203. .226 /note= "MTCS contains a modification of at least one amino acid residue in this region"

FT Region 230. .244 /note= "MTCS contains a modification of at least one amino acid residue in this region"

FT Misc-difference 289 /note= "encode aby ATT"

WO200212537-A2.

XX PR 02-AUG-2000; 2000CN-00119553.

XX PR 18-JAN-2001; 2001CN-00103102.

XX PR (BBIJ-) BEIJING STM BIOTECH LTD.

PA (KEYY/) KE Y.

PA (NIEH/) NIE H.

XX PI Ke Y, Nie H;

XX DR WPI; 2002-227165/28.

XX DR N-PADB; ABA95171.

PT Mutant trichosanthin protein of low antigenicity useful for treating tumor e.g. leukemia, comprises a sequence of native trichosanthin with modification of at least one amino acid residue in three specific regions.

XX Example 1; Fig 1; 42pp; English.

XX The invention relates to a mutant trichosanthin (MTCS) protein of low antigenicity comprising a sequence of native TCS with the modification of at least one amino acid residue in three regions which is 174-180, 203-227 and 230-244 and substantially retaining the biological activities of the native TCS. The MTCS protein, its fragment or derivative is useful as an therapeutic agent; or for preparing a medicament for treating viral disease e.g. acquired immunodeficiency syndrome (AIDS), tumour e.g. The disease, for inducing abortion and/or treating ectopic pregnancy. The present sequence represents the native TCS

SQ Sequence 289 AA;

DB 24 DVSPRLSGATSSSYGVFTSNLRKALPWERKLYDPLRLSSPGSQRVALIHLTNYADETI 83

QY 61 SVAIDVTVVYIMGRADTSYFNEASATEAKYVFDAMRKVTLPSGNVERLQTAGK 120

DB 84 SVAIDVTVVYIMGRADTSYFNEASATEAKYVFDAMRKVTLPSGNVERLQTAGK 143

DB 121 IRENIPGLPGLDA5TTLFYVNAANSASALMVLQTSSEARYKFTFQQIGKRVDTKFL 180

DB 144 IRENIPGLPGLDA5TTLFYVNAANSASALMVLQTSSEARYKFTFQQIGKRVDTKFL 203

DB 181 PSIAIILSLENSALSA5TQIOLSTNNQFESPVLINANQDORVITNDAGVTSNALL 240

DB 204 PSLAIIISLENSALSA5TQIOLASTNNQFESPVLINANQDORVITNDAGVTSNALL 263

QY 241 LNRRNMA 247

DB 264 LNRRNMA 270

RESULT 8

ID ARR67359 standard; protein; 247 AA.

XX AC ARR67359;

XX DT 25-MAR-2003 (revised)

XX DT 26-JUL-1995 (first entry)

XX DE Trichosanthin antiviral protein.

XX KW Antiviral agent; trichosanthin; HIV; hepatitis virus.

XX OS Trichosanthes kirilowii.

XX PN WO9426898-A1.

XX PD 24-NOV-1994.

XX PR 17-MAY-1994; 94WO-CN000037.

XX PR 19-MAY-1993; 93CN-00112436.

XX PA (SHAN-) SHANGHAI INST ORGANIC CHEM.

XX PI Chen H, Xia Y, Jiang K, Bao J;

XX DR WPI; 1995-006794/01.

XX DR N-PADB; AAQ75305.

XX PT New genetically engineered gene for trichosanthin protein - expressed in E.coli, used to produce the protein for use as antiviral agent against HIV and hepatitis virus.

XX CS Claim 1; Fig 1; 37pp; Chinese.

XX AAQ75305 encodes ARR67359 an antiviral protein isolated from the roots of Trichosanthes kirilowii. The trichosanthin antiviral protein is useful for controlling viral infections such as HIV and hepatitis. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 247 AA;

Query Match 99.8%; Score 1218; DB 2; Length 247;

Best Local Similarity 99.6%; Pred. No. 1.8e-10; Mismatches 1; Indels 0; Gaps 0;

Matches 246; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSPRLSGATSSSYGVFTSNLRKALPWERKLYDPLRLSSPGSQRVALIHLTNYADETI 60

DB 1 DVSPRLSGATSSSYGVFTSNLRKALPWERKLYDPLRLSSPGSQRVALIHLTNYADETI 60

QY 61 SVAIDVTVVYIMGRADTSYFNEASATEAKYVFDAMRKVTLPSGNVERLQTAGK 120

DB 61 SVAIDVTVVYIMGRADTSYFNEASATEAKYVFDAMRKVTLPSGNVERLQTAGK 120

RESULT 9

AAR0714

ID AAR07514 standard; protein; 289 AA.

XX

AC AAR07514;

XX

DT 06-FEB-1991 (first entry)

DE Trichosanthin from *Trichosanthes kirilowii*.

XX

KW trichosanthin (TCS); Human immunodeficiency Virus; inhibition.

OS

FH

FT Key

Region

1..21

/label= "signal peptide"

/note= "hydrophobic"

XX

W09012097-A.

XX

PN

18-OCT-1990.

XX

PP 04-APR-1989; 89US-00333184.

XX

PR 04-APR-1989; 89US-00333184.

XX

PA (GENE-) GENLABS INC.

XX

PT Piatek M, Chow T, Fry K;

XX

DR WPI; 1990-334847/44.

XX

N-PSDB; AAQ06343.

XX

PT Recombinant tri-chiosanthin protein - with selective inhibitory effect on viral expression in HIV infected T-cells or monocyte-macrophage.

XX

PS Example; Fig 4; 102pp; English.

XX

CC Genomic DNA was isolated from *T.kirilowii* leaves from Korea and a library was constructed. Clone pQ21D was identified as likely to contain a TCS-encoding sequence in its 4kb insert. The deduced amino acid sequence is identical to that of TCS purified from Cantonese *T.kirilowii* roots, except for 2 conservative substitutions, i.e. Thr for Ser at position 211 and Met for Thr at position 224. The Canton protein lacks the last 19 C-terminal amino acid residues. See also AAQ06344-Q06351.

XX

SQ Sequence 289 AA;

Query Match 99.3%; Score 1212; DB 2; Length 289;

Best Local Similarity 99.2%; Pred. No. 8; 5e-110; Mismatches 1; Indels 0; Gaps 0;

Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRISGATSSYGVFISNLKALPNERKLYDIPLLRSPLSGSQRVALHINTVADETI 60

QY 24 DVSFRISGATSSYGVFISNLKALPNERKLYDIPLLRSPLSGSQRVALHINTVADETI 83

QY 61 SVAIDVNVVYKGRADTSYFNEASATEAKVVFQDAMKVTLPYSGNVERLQTAAGK 120

Db 121 IRENIPGLPLPALSAITLTYNANSASALMVLQTSBARYKIEBQIGKRVDTKFL 180

Db 121 IRENIPGLPLPALSAITLTYNANSASALMVLQTSBARYKIEBQIGKRVDTKFL 180

Db 121 IRENIPGLPLPALSAITLTYNANSASALMVLQTSBARYKIEBQIGKRVDTKFL 180

Db 144 IRENIPGLPLPALSAITLTYNANSASALMVLQTSBARYKIEBQIGKRVDTKFL 203

QY 181 PSLAISLENSNSALSKQIOLASTNGQFESPVVLINAQNQRTITNVDAGVTSNIAL 240

Db 181 PSLAISLENSNSALSKQIOLASTNGQFESPVVLINAQNQRTITNVDAGVTSNIAL 240

QY 241 LNRNNMA 247

Db 241 LNRNNMA 247

Db 241 LNRNNMA 247

Db 264 LNRNNMA 270

RESULT 10

AAR25572

ID AAR25572 standard; protein; 289 AA.

XX

AC AAR25572;

XX

DT 25-MAR-2003 (revised)

DR 13-JAN-1993 (first entry)

XX

DE Trichosanthin from *Trichosanthes kirilowii*.

XX

KW TCS; alpha-trichosanthin; Radix trichosanthin; abortifacient; ribosome inactivating protein; RIP; HIV-infected human T cells; human immunodeficiency virus.

XX

OS Trichosanthes kirilowii.

XX

FH Key

FT Location/Qualifiers

FT Misc-difference 57

FT /note= "Ile in previously published sequence"

FT Misc-difference 60

FT /note= "Ile in previously published sequence"

FT Misc-difference 72

FT /note= "Ile in previously published sequence"

FT Misc-difference 82..84

FT /note= "Region not present in previously published sequence"

FT Misc-difference 92..93

FT /note= "previously published sequence contained a 10 amino acid insert (DAGLPRNAV) between Val and Tyr"

FT Misc-difference 143

FT /note= "Gly in previously published sequence"

FT Misc-difference 144

FT /note= "Leu in previously published sequence"

FT Misc-difference 196

FT /note= "Ser in previously published sequence"

FT Misc-difference 214..215

FT /note= "previously published sequence contained a Leu inserted between Ser and Trp"

FT Misc-difference 216

FT /note= "Leu in previously published sequence"

FT Misc-difference 231

FT /note= "Thr in previously published sequence"

FT Misc-difference 234

FT /note= "Ser in directly sequenced TCS"

FT Misc-difference 246..266

FT /note= "21 amino acids not present in previously published sequence"

FT Misc-difference 247

FT /note= "Thr in directly sequenced TCS"

DN US5128460-A.

XX

DN 07-JUL-1992.

XX

PR 04-APR-1990; 89US-0050475.

PR 04-APR-1989; 89US-00333184.

PR	KW	TCS; alpha-trichosanthin; Radix-trichosanthin; primer; inhibition;
XX	KW	viral expression; HIV; T-cell; macrophage.
PA	XX	
XX	OS	Synthetic.
PI	XX	
XX	FH	Location/Qualifiers
DR	FT	1. .23
XX	FT	/label= "sig_peptide"
PT	FT	/note= "putative N-terminal extension of the mature TCS"
PT	FT	24. .270
PT	FT	/label= mat_protein
PT	FT	Misc-difference 234
XX	FT	/note= "plant-derived TCS has Ser at this position"
PS	FT	270. .289
XX	FT	/note= "putative C-terminal extension of the mature TCS"
CC	FT	US5166056-A.
CC	FT	24-NOV-1992.
CC	FT	09-DEC-1991; 89US-00804293.
CC	PR	04-APR-1989; 89US-00333184.
CC	PR	07-SEP-1989; 89US-00404326.
CC	XX	
CC	PA	(GENE-) GENELABS INC.
CC	PI	Piatak M, Chow TP,
CC	XX	
CC	DR	WPI; 1992-414954/50.
CC	XX	
CC	PS	Recombinant Trichosanthin protein prodn. in E. coli - for use in the selective inhibition of viral expression in HIV infected cells.
XX	PS	Disclosure; Fig 4; 37pp; English.
CC	CC	The sequence is identical to that of plant-derived TCS except for two conservative changes: a Thr for a Ser substitution at position 211 and a Met for a Thr substitution at position 224. TCS is likely produced as a secreted protein that undergoes post-translational processing at both the amino and carboxy ends. The TCS coding sequence was amplified using the primers of AAQ31828-30. The amplified prod. has the sequence of AAQ31827, which was used as a prob. One isolate, P021D, comprises the sequence of AAQ31826. The recombinant TCS sequence may be used in the recombinant prodn. of TCS. TCS can be used for the selective inhibition of viral expression in HIV-infected human T-cells or macrophages. (Updated on 25-MAR-2003 to correct PF field.)
CC	XX	
CC	SQ	Sequence 289 AA;
CC	CC	Query Match 99.3%; Score 1212; DB 2; Length 289;
CC	CC	Best Local Similarity 99.2%; Pred. No. 8.5e-10; Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	CC	
1	CC	DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPURSSLPSQSYVALIHLTYADTTI
24	CC	DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPURSSLPSQSYVALIHLTYADTTI
61	CC	SVAIDVTNVIYMGYRAGDTSYFNEASATEAKVVFQDAMRKVTLPLPSQSYVALIHLTYADTTI
62	CC	SVAIDVTNVIYMGYRAGDTSYFNEASATEAKVVFQDAMRKVTLPLPSQSYVALIHLTYADTTI
84	CC	SVAIDVTNVIYMGYRAGDTSYFNEASATEAKVVFQDAMRKVTLPLPSQSYVALIHLTYADTTI
121	CC	IRENIPLGLPALSATITLYFVNNAASALMVLQIOTSEARRYKFIHQIGKRVDKTFI
180	CC	IRENIPLGLPALSATITLYFVNNAASALMVLQIOTSEARRYKFIHQIGKRVDKTFI
144	CC	IRENIPLGLPALSATITLYFVNNAASALMVLQIOTSEARRYKFIHQIGKRVDKTFI
181	CC	PSLAISLNSWALSALKOIQIASTNGQFETPVVLINAOQNORVMTINYDAGVTSNIALL
204	CC	PSLAISLNSWALSALKOIQIASTNGQFETPVVLINAOQNORVMTINYDAGVTSNIALL
QY	CC	
241	CC	LNRNNMA 247
Db	CC	
264	CC	LNRNNMA 270
RESULT 11	XX	
AAR29272	ID	AAR29272 standard; protein; 289 AA.
XX	AC	AAR29272;
DT	DT	25-MAR-2003 (revised)
DT	DT	16-APR-1993 (first entry)
XX	DE	Trichosanthin protein (encoded by PQ21D).
XX	QY	

Db	264	 LNRNNMMA 270	QY	121	IRENTPLGLPALSATTLFYNAMSASAALMVLQTSBARYKPEEQIGKRUDKTEL 180
RESULT 12			DB	144	IRENTPLGLPALSATTLFYNAMSASAALMVLQTSBARYKPEEQIGKRUDKTEL 203
ID	AAR32886		QY	181	PSLAISLENSWALSKQIQTASTNNGQFSPSPVVLINAQNQRMVITNNVDAQVTSNIAL 240
XX	AAR32986;		DB	204	PSLAISLENSWALSKQIQTASTNNGQFSPSPVVLINAQNQRMVITNNVDAQVTSNIAL 263
AC			QY	241	LNRNNMMA 247
DT	27-AUG-2003	(revised)	DB	264	LNRNNMMA 270
DT	25-MAR-2003	(revised)	DE	17-JUN-1993	(first entry)
XX	Encodes chinese cucumber alpha-tricosanthin.		DE		
XX			DE		
KW	Recombinant products; commercial production; fermentation; biosynthesis;		XX		
KW	natural products; recombinant proteins; product expression; expressed proteins.		XX		
OS	Cucurbitaceae.		XX		
XX			XX		
PN	WO9303161-A1.		AC	AAR55129;	
XX			XX		
DD	18-FEB-1993.		XX		
XX			DT	27-AUG-2003	(revised)
PF	31-JUL-1992;	92WO-US006359.	DT	25-MAR-2003	(revised)
XX			DT	11-JAN-1995	(first entry)
PR	01-AUG-1991;	91US-00739143.	XX		
XX			DE		
PA	(DONS/)	DONSON J.	XX		
PA	(DAWS/)	DAWSON W O.	XX		
PA	(GRAN/)	GRANTHAM G L.	XX		
PA	(TURP/)	TURPEN T H.	OS		
PA	(TURP/)	TURPEN A M.	Trichosanthes kirilowii.		
PA	(GARG/)	GARGER S J.	XX		
PA	(GRIL/)	GRILLE L K.	XX		
XX			XX		
FI	Donson J, Dawson WO, Grantham GL, Turpene TH, Turpene AM;		XX		
PI	Garger SJ, Grille LK;		XX		
XX			XX		
DR	WPI; 1993-076518/09.		XX		
DR	N-PSDB; AA037679.		XX		
XX			XX		
PT	Recombinant plant viral nucleic acids - used to express a prod., e.g.		XX		
PT	antibody or IL-1 in a plant.		XX		
XX			XX		
PS	Example 4; Page 96; 30pp; English.		XX		
XX			XX		
CC	This sequence represents chinese cucumber alpha-tricosanthin. The coding		XX		
CC	sequence is inserted into a recombinant plant viral nucleic acid which is		XX		
CC	then used to express a recombinant product (in this case alpha-		XX		
CC	tricosanthin) in a plant. The plant viral sequence may be from tobacco		XX		
CC	mosaic, cucumber green mottle, cowpea mosaic, bromo mosaic, broad bean		XX		
CC	mottle, rice necrosis, geminiviruses, tomato golden mosaic, Cassava		XX		
CC	latent and mafe streak viruses. (Updated on 25-MAR-2003 to correct PN		XX		
CC	field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-		XX		
CC	2003 to correct PI field.) (Updated on 27-AUG-2003 to correct CS field.)		XX		
SQ	Sequence 289 AA;		XX		
Query Match	99.3%; Score 1212; DB 2; Length 289;		XX		
Best Local Similarity	99.2%; Pred. No. 8; Se-10;		XX		
Matches	245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		XX		
QY	1	DYSLRSGATSSYGVFISNLRKALPMLRKVLDIPLRSLPSQSRVALIHLNYADETI	60		
QY	24	DYSLRSGATSSYGVFISNLRKALPMLRKVLDIPLRSLPSQSRVALIHLNYADETI	83		
DB	61	SYAIDVNVVYMGYRAGDTSYFNEAATTAARCKVFDAMRKVTPYPSGNYRLQTAGK	120		
QY	84	SYAIDVNVVYMGYRAGDTSYFNEAATTAARCKVFDAMRKVTPYPSGNYRLQTAGK	143		
DB	Sequence 289 AA;		XX		
XX			XX		
CC	The alpha-tricosanthin gene may be inserted into a recombinant plant		XX		
CC	virus which can then be used to infect plants for the production of non-		XX		
CC	native products (in this case alpha-tricosanthin). Other genes which		CC		
CC	may be inserted into the virus are those which control a phenotypic		CC		
CC	trait, such as male sterility, or sequences encoding anti-sense RNA which		CC		
CC	can be useful to prevent the expression of undesired phenotypic traits.		CC		
CC	The recombinant virus is derived from a plus sense, single stranded virus		CC		
CC	selected from tobamovirus, bromo mosaic virus, rice necrosis virus or a		CC		
CC	geminivirus. (Updated on 25-MAR-2003 to correct PR field.) (Updated on		CC		
CC	27-AUG-2003 to correct OS field.)		XX		
SQ	Sequence 289 AA;		XX		

XX
 PT Recombinant viral DNA for altering plant phenotype or protein prodn -
 PT contains non-native sub-genomic promoter for expression of heterologous
 PT protein and native promoter for expression of coat protein.
 XX
 PS Example 4; Col 45-46; 42pp; English.

XX
 CC The sequences given in AAW11868-71 represent proteins which were produced
 CC by the recombinant viruses of the invention. The viruses are recombinant
 CC plant viruses which comprise a native plant virus subgenomic promoter, at
 CC least one non-native plant virus subgenomic promoter, and a sequence
 CC encoding a plant virus coat protein. These heterologous sequences are
 CC preferably under the control of the native promoter sequence. By using a
 CC plant virus existing cells can be altered with a new coding sequences
 CC without involving germ cell. The recombinant viruses are stable and can
 CC cause systemic infection, with stable expression/transcription in plants
 CC that are hosts for the non-native part of the vector. The nucleotide
 CC sequences encoding these protein preferably integrated in plant viruses
 CC having either the O-coat protein or the U1-coat protein gene. (Updated on
 CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
 CC field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX

SQ Sequence 289 AA;

Query Match Best Local Similarity 99.3%; Score 1212; DB 2; Length 289;
 Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DVSFRUSGATSSYGVFISNLKALPWERKLYDIPLLRSSLGSGQYALINTNYADETI 60
 Db 24 DVSFRUSGATSSYGVFISNLKALPWERKLYDIPLLRSSLGSGQYALINTNYADETI 83
 Qy 61 SVAIDVTVVYIMYRAGDTSYFNEASATEAAKVFKDAMRKVTLPSGNVRLQTAGK 120
 Db 84 SVAIDVTVVYIMYRAGDTSYFNEASATEAAKVFKDAMRKVTLPSGNVRLQTAGK 143
 Qy 121 IRENIPIGLPLADSATTLFYFTNANSASALAMVLIOTSEARYKFEQGKRVKTFL 180
 Db 144 IRENIPIGLPLADSATTLFYFTNANSASALAMVLIOTSEARYKFEQGKRVKTFL 203
 Qy 181 PSLAITSLENSALSQIOIATNNQOPESPVLINAQNQVITNDASVTSNALL 240
 Db 204 PSLAITSLENSALSQIOIATNNQOPESPVLINAQNQVITNDASVTSNALL 263
 Qy 241 LNRNNA 247
 Db 264 LNRNNA 270

Search completed: April 12, 2005, 15:10:00
 Job time : 112.519 secs

submitted to the Brookhaven Protein Data Bank, July 1994
 A; Reference number: A67092; PDB:1MRK
 A; Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24-27
 R; Xiong, J. P.; Xia, Z. X.; Wang, Y.
 R; Xiong, J. P.; Xia, Z. X.; Wang, Y.
 Nat. Struct. Biol. 1, 695-700, 1994
 A; Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re-submitted to the Brookhaven Protein Data Bank, December 1994
 A; Reference number: A66711; PDB:1TC5
 A; Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27
 R; Xiong, J. P.; Xia, Z. X.; Wang, Y.
 Nat. Struct. Biol. 1, 695-700, 1994
 A; Reference number: A58622; MUID:95360714; PMID:7634073
 A; Contents: annotation; X-ray crystallography, 1.7 angstroms
 C; Comment: Alpha-trichosanthin has been used to induce abortions.
 C; Genetics
 A; Gene: tcs
 C; Function:
 A; Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA ther
 C; Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 C; Keywords: abortifacient; glycosidase; hydrolase; root; toxin
 F; 1-23/Domain: signal sequence #status predicted <SIG>
 F; 24-27/0/Product: trichosanthin alpha #status experimental <MAT>
 F; 27-269/Domain: rRNA N-glycosidase homology <RNG>
 F; 93-183,-86/Active site: Tyr, Glu, Arg #status predicted <CTP>
 Query Match 100.0%; Score 1221; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 3.7e-95;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DVSRFLSGATSSSYGVFISNLRKALPNERKLYDPLRSLPGSQRVALIHLTNYADETI 60
 Db 24 DVSRFLSGATSSSYGVFISNLRKALPNERKLYDPLRSLPGSQRVALIHLTNYADETI 60
 Qy 61 DVSRFLSGATSSSYGVFISNLRKALPNERKLYDPLRSLPGSQRVALIHLTNYADETI 60
 Db 121 IRENIPGLPALSATTLFYNNANSASALMVLQTSRSARYKFEIQQIGKRVDTKFL 180
 Qy 121 IRENIPGLPALSATTLFYNNANSASALMVLQTSRSARYKFEIQQIGKRVDTKFL 180
 Db 181 PSLATISLENSWALSQKQILASTNGQFSPVVLINAQNQRTITNDAGVTSNIAL 240
 Qy 181 PSLATISLENSWALSQKQILASTNGQFSPVVLINAQNQRTITNDAGVTSNIAL 240
 Db 181 PSLATISLENSWALSQKQILASTNGQFSPVVLINAQNQRTITNDAGVTSNIAL 240
 Qy 241 LNRNNA 247
 Db 241 LNRNNA 247

RESULT 3

JC5606
 Karasurin C - Trichosanthes kirilowii var. japonica

N; Contains: karasurin A
 C; Species: Trichosanthes kirilowii var. japonica
 C; Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
 C; Accession: JC5606; JCB033
 R; Mizukami, H.; Tida, K.; Kondo, T.; Ogihara, Y.
 Biol. Pharm. Bull. 20, 711-713, 1997
 A; Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating prote
 A; Reference number: JC5606; MUID:9735662; PMID:9212998
 A; Accession: JC5606
 A; Molecule type: DNA
 A; Residues: 1-289 <MIZ>
 A; Cross-references: UNIPROT:P24478; DDBJ:AB000666; NID:92329830; PID:BA21786.1; PID:g2
 R; Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
 Biol. Pharm. Bull. 19, 1485-1489, 1996
 A; Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka
 A; Reference number: JCB032; MUID:97108848; PMID:8951169
 A; Accession: JCB032
 A; Status: Preliminary
 A; Molecule type: protein
 A; Residues: 22-270 <KON>
 C; Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti
 C; Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 F; 24-27/0/Product: Karasurin C #status predicted <MAC>
 F; 27-269/Domain: rRNA N-glycosidase homology <RNG>
 F; 27-269/Domain: rRNA N-glycosidase homology <RNG>

Query Match 97.8%; Score 1194; DB 2; Length 289;
 Best Local Similarity 97.6%; Pred. No. 6.9e-93;
 Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DVSRFLSGATSSSYGVFISNLRKALPNERKLYDPLRSLPGSQRVALIHLTNYADETI 60
 Db 24 DVSRFLSGATSSSYGVFISNLRKALPNERKLYDPLRSLPGSQRVALIHLTNYADETI 60
 Qy 61 DVSRFLSGATSSSYGVFISNLRKALPNERKLYDPLRSLPGSQRVALIHLTNYADETI 60
 Db 121 IRENIPGLPALSATTLFYNNANSASALMVLQTSRSARYKFEIQQIGKRVDTKFL 180
 Qy 121 IRENIPGLPALSATTLFYNNANSASALMVLQTSRSARYKFEIQQIGKRVDTKFL 180
 Db 181 PSLATISLENSWALSQKQILASTNGQFSPVVLINAQNQRTITNDAGVTSNIAL 240
 Qy 181 PSLATISLENSWALSQKQILASTNGQFSPVVLINAQNQRTITNDAGVTSNIAL 240
 Db 204 PSLATISLENSWALSQKQILASTNGQFSPVVLINAQNQRTITNDAGVTSNIAL 240
 Qy 241 LNRNNA 247

RESULT 2

JU0393
 karasurin - Mongolian snake-gourd

C; Species: Trichosanthes kirilowii (Mongolian snake-gourd)

C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C; Accession: JU0393; PS0153
 R; Torokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.
 Chem. Pharm. Bull. 39, 1244-1249, 1991
 A; Title: The complete amino acid sequence of an abortifacient protein, karasurin.
 A; Reference number: JU0393; MUID:92005921; PMID:1914000
 A; Accession: JU0393
 A; Residues: 1-247 <TO>
 A; Molecule type: protein
 A; Residues: 1-247 <TO>
 A; Cross-references: UNIPROT:P24478
 A; Note: a sequence which lacks Ala-247 is also shown in this publication
 C; Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 C; Keywords: abortifacient

Query Match 97.8%; Score 1194; DB 2; Length 247;

Best Local Similarity 97.6%; Pred. No. 5.5e-93;

Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 264 LNRNMA 270

RESULT 4

C:Species: Trichosanthes kirilowii var. japonica

C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004

C:Accession: JC5032

R:Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.

Biol. Pharm. Bull. 19, 1485-1489, 1996

A:Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka

A:Reference number: JC5032; MUID:97108848; PMID:8951169

A:Status: preliminary

A:Residues: 1-247 <KON>

A:Cross-references: UNIPROT:Q41216; UNIPROT:Q94KE4; UNIPROT:Q8LW7

C:Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyti

C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology <RNG>

F:4-243/Domain: rRNA N-glycosidase

Query Match Similarity 97.4%; Score 1189; DB 2; Length 247; Matches 240; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DVSRPLSGATSSSYGVFTSNRKALPNERKLYDPLRSSLPSQSYRVALIHLTNYADETI 60

Db 1 DVSPRLSGATSSSYGVFTSNRKALPNERKLYDPLRSSLPSQSYRVALIHLTNYADETI 60

Qy 61 SVAIDVTNIVYIMGRAGTSYFVNNEASATEAAKVKVFDAMRKVTLPYSGNYERLQTAAGK 120

Db 61 SVAIDVTNIVYIMGRAGTSYFVNNEASATEAAKVKVFDAMRKVTLPYSGNYERLQTAAGK 120

Qy 121 IRENIPGLPAUDSAITLFLYVYANSAASALMVLQIOTSEAAKVKFISQOIGKRVDKPFL 180

Db 121 IRENIPGLPAUDSAITLFLYVYANSAASALMVLQIOTSEAAKVKFISQOIGKRVDKPFL 180

Qy 181 PSLAISLENSWALKSKOIQIOLASTNNQFESPVULINQNRVITNDAGVTSNIAL 240

Db 181 PSLAISLENSWALKSKOIQIOLASTNNQFESPVULINQNRVITNDAGVTSNIAL 240

Qy 241 LNRNMA 247

Db 241 LNRNMA 247

RESULT 5

RLPUGG rRNA N-glycosidase (EC 3.2.2.22) alpha-momorcharin precursor [validated] - balsam Pear

N:Alternative names: agglutinin; momordin-A; ribosome-inactivating protein momorcharin alp

C:Species: Momordica charantia (balsam pear, bitter gourd)

C:Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 09-Jul-2004

C:Accession: S14273; A61318; S61318; S61649; S61570

R:Ho, W.K.K.; Liu, S.C.; Shaw, P.C.; Yeung, H.W.; Ng, T.B.; Chan, W.Y.

Biochim. Biophys. Acta 1088, 311-314, 1991

A:Title: Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating protein.

A:Reference number: S14273; MUID:91159486; PMID:2001404

A:Accession: S14273

A:Residues: 1-286 <HOW>

A:Cross-references: UNIPROT:P16094; EMBL:X57682; NID:919527; PIDN:CAA40869.1; PID:91528

R:Liu, S.S.L.

Experientia 36, 524-527, 1980

A:Title: Purification and partial characterization of two lectins from Momordica charant

A:Reference number: A61318; MUID:82021763; PMID:7379938

A:Accession: A61318

A:Molecule type: protein

A:Residues: 24-50 <LIA>

A:Note: a lectin shows agglutinating activity for type-O red blood cells

R:Montecuccuzzi, P.C.; Lazzarini, A.M.; Barberi, L.; Stirpe, F.; Soria, M.; Lappi, D.

Int. J. Pept. Protein Res. 33, 247-1989

A:Title: N-terminal sequence of some ribosome-inactivating proteins.

A:Reference number: S16331; MUID:89326691; PMID:2733596

A:Accession: S1640

A:Molecule type: Protein

A:Residues: 24-68, 'X', 70 <MON>

R:Minami, Y.; Funatsu, G.

Biceci, Biotechnol. Biochem. 57, 1141-1144, 1993

A:Title: The complete amino acid sequence of momordin-a, a ribosome-inactivating protein.

A:Reference number: JN0628; MUID:9337245; PMID:7763984

A:Accession: JN0628

A:Molecule type: protein

A:Residues: 24-107, 'O', 109-123, 125-147, 'L', 149-154, 'I', 156-205, 'I', 207-208, 'L', 210-214,

R:Ren, J.; Wang, Y.; Dong, Y.; Stuart, D.I.

R:submitted to the Brookhaven Protein Data Bank, January 1994

A:Reference number: A62272; PDB:1AHC

A:Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 24-269

R:Hubain, J.; Tickle, I.J.; Wood, S.P.

R:submitted to the Brookhaven Protein Data Bank, March 1994

A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA the

C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-23/Domain: amino-terminal propeptide #status predicted <PRO>

F:24-269/Domain: rRNA N-glycosidase alpha-momorcharin #status experimental <MAT>

F:27-266/Domain: rRNA N-glycosidase homology <RNG>

F:270-286/Domain: carbohydrate-terminal propeptide #status Predicted <CTP>

F:250/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match Similarity 65.7%; Score 802; DB 1; Length 206; Matches 161; Conservative 37; Mismatches 49; Indels 0; Gaps 0;

Qy 1 DVSPRLSGATSSSYGVFTSNRKALPNERKLYDPLRSSLPSQSYRVALIHLTNYADETI 60

Db 24 DVSPRLSGATSSSYGVFTSNRKALPNERKLYDPLRSSLPSQSYRVALIHLTNYADETI 60

Qy 61 SVAIDVTNIVYIMGRAGTSYFVNNEASATEAAKVKVFDAMRKVTLPYSGNYERLQTAAGK 120

Db 24 DVSPRLSGATSSSYGVFTSNRKALPNERKLYDPLRSSLPSQSYRVALIHLTNYADETI 60

Qy 61 SVAIDVTNIVYIMGRAGTSYFVNNEASATEAAKVKVFDAMRKVTLPYSGNYERLQTAAGK 120

Db 84 TVAVDVTNIVYIMGRAGTSYFVNNEASATEAAKVKVFDAMRKVTLPYSGNYERLQTAAGK 143

Qy 121 IRENIPGLPAUDSAITLFLYVYANSAASALMVLQIOTSEAAKVKFISQOIGKRVDKPFL 180

Db 144 PREKIPIGLPAUDSAITLFLYVYANSAASALMVLQIOTSEAAKVKFISQOIGKRVDKPFL 180

Qy 181 PSLAISLENSWALKSKOIQIOLASTNNQFESPVULINQNRVITNDAGVTSNIAL 240

Db 204 PSLAISLENSWALKSKOIQIOLASTNNQFESPVULINQNRVITNDAGVTSNIAL 240

Qy 241 LNRNMA 247

Db 264 LNRNMA 270

RESULT 6

C:Species: Luffa cylindrica (smooth loofah)

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004

C:Accession: S22494; S26390; JTO202; A32842

R:Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.

Plant Mol. Biol. 18, 119-120, 1992

A:Reference number: S22494; MUID:9228831; PMID:1600156

A:Accession: S22494

A;Molecule type: mRNA
 A;Residues: 1-277 <RAT>
 A;Cross-references: UNIPROT:Q00465; EMBL:X62371; NID:919145; PIDN:CAA44229.1; PID:919146
 R;Islam, M.R.; Nishida, H.; Funatsu, G.
 Agric. Biol. Chem. 54, 2967-2979, 1990
 A;Title: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from
 A;Reference number: S26390; MUID:91248471; PMID:1368651
 A;Accession: S26390
 A;Molecule type: protein
 A;Residues: 21-53, 'L', '55', 'I', '57-86, 'SQL', 90-154, 'L', 156-157, 'I', 159-173, 'L', 175-209, 'SL'
 R;Islam, M.R.; Nishida, H.; Funatsu, G.
 Agric. Biol. Chem. 54, 1343-1345, 1990
 A;Title: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from
 A;Reference number: JH0202; MUID:91197482; PMID:1368623
 A;Molecule type: protein
 A;Accession: JH0202
 A;Residues: 21-53, 'L', '55', 'I', '57-86, 'SQL', 90-154, 'L', 156-157, 'I', 159-173, 'L', 175-209, 'SL'
 R;Ramakrishnan, S.; Englund, J.J.; Bryant Jr., H.L.; Xu, F.J.
 Biochem. Biophys. Res. Commun. 160, 509-516, 1989
 A;Title: Characterization of a translation inhibitory protein from *Luffa aegyptiaca*.
 A;Reference number: A32542; MUID:89246493; PMID:2719679
 A;Accession: A32542
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 21-28, 'G', 30, 'X', 32-34, 'K', 36-40 <RAM>
 C;Function:
 A;Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA ther
 C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase; homology
 C;Keywords: glycoprotein; glycosidase; hydrolase; seed; toxin
 F;1-260/Domain: signal sequence #status predicted <SIG>
 F;21-262/Domain: rRNA N-glycosidase alpha-luffin #status experimental <MAT>
 F;24-262/Domain: rRNA N-glycosidase homology <RNG>
 F;26-277/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F;48-53, 97-104, 225, 246/Binding site carbohydrate (Asn) (covalent) #status experimental
 F;90-179, 182/Active site: Tyr, Glu, Arg #status predicted

Query Match 61.8%; Score 754; DB 2; Length 277;
 Best Local Similarity 62.1%; Pred. No. 6, 3e-56;
 Matches 154; Conservative 42; Mismatches 50; Indels 2; Gaps 2;

QY 1 DVSPRLSGATSSSYGVFISNRKALPWERKLYDIPRLRSSLPGSQRVALIHLNTYADETI 60
 21 DYRFSLGSSSSSYSKFQDILKALPENGTVNITLSSASAGASRVTMLTMSYDKA 80
 Db 61 SVAIDVNVVYMGYRAGTSYFNEASAATEAKVFKDAMRKVTPYPSGNVRLQTAGK 120
 81 'YVAVDVNVVYMGYVLYVASTSYFNEFSDAKLQSYQVKGS-TIVLPLPSGNVRLQTAGK 139
 QY 121 IRENIPGLPALSAITLFLYNNANSASALMVLQSTSBEARYKPIEQQIGKRVDTKFL 180
 140 IREKIPGLPALSAITLFLYHDTAAAFALVYIOTTAESRFPKVYEGQIERTKSNQV 199
 QY 181 PSALATISLENSWNSALSKQIQLASTNGQFESPVVLIMAQNQRTITNDAGVTSNIAL 240
 200 PSALATISLENSWNSALSKQIQLAQTNQGTFKTPVWITDDKGQRVEITNVTSKVTKNIQLL 259
 QY 241 LN-RNNA 247
 Db 260 LNPKQNTA 267

RESULT 8
 S25560
 rRNA N-glycosidase (EC 3.2.2.22) momordin II - balsam apple
 C;Species: Momordica balsamina (balsam apple)
 C;Date: 22-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C;Accession: S25560
 R;Ortigao, M.; Better, M.
 A;Title: Momordin II, a ribosome inactivating protein from *Momordica balsamina*, is homologous to the ribosome inactivating protein from *Momordica charantia*.
 A;Reference number: S25560; MUID:93027170; PMID:1408771
 A;Accession: S25560
 A;Molecule type: preliminary
 A;Residues: 1-266 <ORT>
 A;Cross-references: UNIPROT:P29339; EMBL:Z12175; NID:919525; PIDN:CAA78166.1; PID:919526
 C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 C;Keywords: glycosidase; hydrolase
 F;27-264/Domain: rRNA N-glycosidase homology <RNG>
 Query Match 58.1%; Score 709; DB 2; Length 286;
 Best Local Similarity 61.6%; Pred. No. 4e-52;
 Matches 149; Conservative 30; Mismatches 61; Indels 2; Gaps 2;

QY 1 DVSPRLSGATSSSYGVFISNRKALPWERKLYDIPRLRSSLPGSQRVALIHLNTYADETI 60
 24 DVNFDISTATAKTYKTFIEDFATLPSHVKYDIPLYSTISDSRKFILDLTSAYETI 83
 QY 61 SVAIDVNVVYMGYRAGTSYFNEASAATEAKVFKDAMRKVTPYPSGNVRLQTAGK 120
 84 SVAIDVNVVYAYRTRDVSYFKE-SPEAYNLFK-GTRKIKLPTYGNENLQTAHK 141
 Db 121 IRENIPGLPALSAITLFLYNNANSASALMVLQSTSBEARYKPIEQQIGKRVDTKFL 180
 142 IRENIPGLPALSAITLFLYNNANSASALMVLQSTSBEARYKPIEQQIGKRVDTKFL 201
 QY 181 PSALATISLENSWNSALSKQIQLASTNGQFESPVVLIMAQNQRTITNDAGVTSNIAL 240
 202 PSALATISLENSWNSALSKQIQLAQTNQGTFKTPVWITDDKGQRVEITNVTSKVTKNIQLL 261
 QY 241 LN 242
 Db 262 LN 263

RESULT 7
 S23519
 beta-luffin - smooth loofah
 C;Species: *Luffa cylindrica* (smooth loofah)
 C;Accession: S23519; S23113
 R;Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
 Plant Mol. Biol. 19, 887-889, 1992
 A;Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating protein
 A;Reference number: S23519; MUID:9253400; PMID:1633290
 A;Accession: S23519

Db	61	TVAVDVTVVTVAYRADAVYFFEDTPA-EAKLIFA-GTKWKLPIVSGNVDLQSYVKG	118	A; Reference number: A48237; MUID: 91352006; PMID: 1881883
Qy	121	IRENPPIGLPLAQLSAITLFLYNNANSASALMVLQIOTSEARYKFLFEOQKGRVKDVKFL	180	A; Contents: annotation; active site
Db	119	QRMIELGIPALSSAITNNVYDQYSTAALVLQISPAEARYKVEQQVSHISNFY	178	A; Rutenber, E.; Robertus, J.D.
Qy	181	PSALIISLENSALSKOIQIA-TNNQPEVSVLINAQNQRTVITNVADWTSIAL	239	A; Title: Structure of ricin B-chain at 2.5 angstrom resolution.
Db	179	PNOAVISLENKGALSKOIQIA-NRTGHQFENVELYNPDGTRFSVHTSAGVKGNIK	238	A; Reference number: A48238; MUID: 91352005; PMID: 1881882
Qy	240	LL 241		A; Contents: annotation; X-ray crystallography, 2.5 angstroms
Db	239	LL 240		R; Kazarin, B.J.; Collins, B.J.; Robertus, J.D.
RESULT 12				
RLCSD				
Ricin D precursor - castor bean				
N; Contains: rRNA N-glycosidase (EC 3.2.2.22)				
C; Species: Ricinus communis (castor bean)				
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004				
C; Accession: A24041; S20513; A24614; A03372; A24010; A03374; S1003				
R; Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.				
Nucleic Acids Res. 13, 819-833, 1985				
A; Title: Genomic cloning and characterization of a ricin gene from <i>Ricinus communis</i> .				
A; Reference number: A24041; MUID: 86067214; PMID: 2999712				
A; Residues: 1-576 <HAL>				
A; Molecule type: DNA				
A; Cross-references: UNIPROT: P02879; GB:X03179; NID: 921082; PIDN: CAA26939.1; PID: 921083				
A; Reference: J.W.; Roberts, L.M.				
A; Title: The lectin gene family of <i>Ricinus communis</i> : cloning of a functional ricin gene				
A; Reference number: S20513; MUID: 92163016; PMID: 1371405				
A; Accession: S20513				
A; Molecule type: DNA				
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A; Cross-references: EMBL: X52908; NID: 921084; PIDN: CAA37095.1; PID: 921085				
A; Reference: R.; Lamb, J.T.; Roberts, L.M.; Lord, J.M.				
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A; Molecule type: DNA				
A; Residues: 1-576 <HAL>				
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A; Reference: R.; Lamb, J.T.; Roberts, L.M.; Lord, J.M.				
A; Accession: S20513				
A; Molecule type: DNA				

A;Title: The complete amino acid sequence of the B-chain of the *Ricinus communis* agglutinin. Accession number: A24210

A;Molecule type: protein

C;Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-554

C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared to ricin.

C;Superfamily: ricin; rRNA N-glycosidase homology

C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-290/Product: agglutinin chain A #status predicted <ACH>

F;35-281/Domain: rRNA N-glycosidase homology <RNG>

F;303-564/Product: agglutinin chain B #status experimental <BCB>

F;319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats

F;34,259/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;104,1-7,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted

F;200,203/Active site: Glu, Arg #status predicted

F;282-306,322-341,345-366,492-509/Disulfide bonds: #status predicted

F;324-337,438/Binding site: N-acetylgalactosamine (Asp, Glu, Asn) #status predicted

F;397,437/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;536,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

Query Match 32.5%; Score 396.5; DB 1; Length 564;

Best Local Similarity 37.3%; Pred. No. 1.9e-25;

Matches 95; Conservative 55; Mismatches 86; Indels 19; Gaps 9;

Qy 2 VSFRISGATSSSYGVVINSRKLKALPWERKL-YDIPIL--RSSLPGSORYALHLNTYADE 58

Db 33 INFTRADATIVESYNTNFTRAVRSHLTGADVRHEIPVLPNRLVGPISORFLVLSNHRL 92

Qy 59 TISVAIDVNTVNYIMSGRAGTSYF--NEASATTAALKVFKDAMRKUTLPVSGNYRLQ 115

Db 93 SVTLLADLVNAYVVGTRAGNSAYFHPDNQEDA-BATHLFTDVQNSFTFAGGNVYRL 151

Qy 116 TAGKIKRNTPLGLPAILDSAITTFLYNA-----NSAASALMVTQTSSEARVYKPEQQ 170

Db 152 QLGG-LRNEIPLGTPLEDAISALYYIYSTCTGQIPTLARSFMVCIQTMSEARFFQYIEG 210

Qy 171 IGKRV--DKTFLPLSLAISLENSWMSLSKQIQTASTNGQFESPWVILNAQMQRVITNV 228

Db 211 MRTRRYNRSSAPDPVSITLENSWGRUSTAIQ--ESNQGAFASPIQLORRNGSKFNV--Y 266

Qy 229 DAGVTTSNIAILLNKR 243

Db 267 DVSILIPPIALMVYR 281

RESULT 14

C39761 abrin (clone 7.2) precursor - Indian licorice (fragment)

N-Contains: rRNA N-glycosidase (EC 3.2.2.22)

C;Species: Abrus precatorius (Indian licorice)

C;Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: C39761; S1471

R;Evensen, G.; Matthesen, A.; Sundan, A.

R; Biol. Chem. 266: 6843-6852, 1991

A;Title: Direct molecular cloning and expression of two distinct abrin A-chains. Accession number: A39761; PMID:91201329; PMID:2016300

A;Molecule type: DNA

A;Residues: 1-251 <EVE>

A;Cross-references: UNIPROT:Q38760

R;Evensen, G.; Matthesen, A.; Sundan, A. submitted to the EMBL Data Library, October 1990

A;Description: Direct molecular cloning of two distinct abrin A-chains. Reference number: S1471

A;Accession: S14471

A;Molecule type: DNA

A;Residues: 'M',1-251 <EV2>

A;Cross-references: EMBL:X54872; NID:gi16088; PIDN:CAA38654.1; PID:gi16089

C;Superfamily: ricin; rRNA N-glycosidase homology

C;Keywords: duplication; glycosidase; hydrolase; lectin; toxin

F;1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>

F;7-246/Domain: rRNA N-glycosidase homology <RNG>

F:174,113,195,196/Active site: Glu, Arg #status predicted
 Query Match 28.8%; Score 352; DB 2; Length 251;
 Best Local Similarity 38.6%; Pred. No. 3,4e-22;
 Matches 95; Conservative 42; Mismatches 97; Indels 12; Gaps 8;
 Best Local Similarity 37.8%; Pred. No. 5,5e-21; Length 528;
 Matches 93; Conservative 43; Mismatches 98; Indels 12; Gaps 8;
 Query 2 VSRFLSGATSSSGVFSNLKALPNERKLYDPLL-RSSLGQSQRVYLHMTNADET 59
 Db 5 IKRSTEGATQSQYKQFIALRERL-RGGLILHDIPVLRDPTVEERNRYTIVELNSERES 63
 Qy 60 ISVADIVMVVYRAGDTSTFNEPESATEAKVYFKDAMRKVTLPLPSGNYEULQTAAG 119
 Db 64 IEVGIDVNVAYVAYRAGSOSYFIRDAPAS-ASTYLFCTQR-YSLRFDSGSYGDIERWAH 121
 Qy 120 KIRENPIGLPAIDSAITL-FYNNANSAASALMVIQSTSEARRYKEIEQQIGK-RV 175
 Db 122 QPREQISLGLQALTHAISFLRSGASNDSEKARTLVIQMASEARRYKVISNRGVSI 181
 Qy 176 DKTFPLSPHAISLNSMNSALKSIQIASTNNGQFESPVYLINAGQNQYRIVTINQAGWTS 235
 Db 182 GTAFQDPDAMLSENNDNLSRQVQ-ESVQDTPPNAVTLRVRVNNQPVIVDSDLTHQSV-A 238
 Qy 236 NIALL 241
 Db 239 VLAIML 244

RESULT 15

S32431 abrin-d precursor - Indian licorice (fragment)
 N-Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C;Species: Abrus precatorius (Indian licorice)
 C;Date: 30-Sep-1993 #sequencing_revision 01-Aug-1997 #text_change 09-Jul-2004
 C;Accession: S32431; S34408
 R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
 J. Mol. Biol. 229, 263-267, 1993
 A;Title: Primary structure of three distinct isoabrinins determined by cDNA sequencing
 A;Reference number: S32429; MUID:93132798; PMID:8421313
 A;Accession: S32431
 A;Molecule type: mRNA
 A;Residues: 1-528 <HUN>
 R;Hung, C.; Lee, M.; Lee, T.; Lin, J.
 Submitted to the EMBL Data Library, March 1993
 A;Accession: S34408
 A;Molecule type: mRNA
 A;Residues: 1-159, 'C' 171-320, 'L' 322-528 <HU2>
 A;Cross-references: GB:MR9346
 C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for tcc
 C;Superfamily: ricin; rRNA N-glycosidase homology
 C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; P1-251/P-product: abrin-d chain A #status predicted <ACH>
 P1-246/Domain: rRNA N-glycosidase homology <RNG>
 P1-261-528/Product: abrin-d chain B #status predicted <BCH>
 P1-283-325,326-365,369-407,414-449,449-492,495-528/Region: 40-residue repeats
 P1/Modified site: pyrroleidone carboxylic acid (Gln) #status predicted
 P1-74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 P1-164,167/active site: Glu, Arg #status predicted
 P1-200,253,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted
 P1-247,269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
 P1-288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
 P1-500,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

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QY 60 ISVALIDTNTVYIMGRAGDTSYIFFNNEASATEAKKYYFKDAMRKVUTPYSGNVERLQTA 119
QY Db 64 IEGVGDIVTNTVYAWTRAGQSOFYLRDAPAS-ASTYLFPGTQR-YSLRFDGYGDLLERWAH 121
QY 120 KIRENPILGLPALDSDAITLE--FVYVANSAASALMWLIQOSTEARQKFISQOIGK--RV 175
QY Db 122 QTRREISLGIQALTAISFLRSAGSANDEBKARTLIVIQMASEARAKYIISRGWSIRT 181
QY 176 DKTFLPLSATISLENSWSALSQKQIATNSTNGQFESPWLINAQNQRTVTNTVDA 235
QY Db 182 GTAFQDPDPAMLSLENNWDNLSSGGVQ--QSVQDTPNPNVILSINTROPVWVUDSLSHPTV-A 238
QY 236 NIALLL 241
QY Db 239 VLAIML 244

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
 US-09-792-793A-39
 Sequence 39, Application US/09792793A
 ; Patent No. US20020168370A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McDonald, John R.
 ; APPLICANT: Coggins, Philip
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
 ; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
 ; FILE REFERENCE: 22020-010D
 ; CURRENT APPLICATION NUMBER: US/09/792,793A
 ; CURRENT FILING DATE: 2001-07-22
 ; NUMBER OF SEQ ID NOS: 93
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 39
 ; LENGTH: 247
 ; TYPE: PRT
 ; ORGANISM: trichosanthus kirilowii
 ; US-09-792-793A-39

Query Match 100.0%; Score 1221; DB 9; Length 247;
 Best Local Similarity 100.0%; Pred. No. 17e-112;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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2	1221	100.0	247	15	US-10-375-209A-39	Sequence 39, Appli
3	1214	99.4	289	11	US-09-905-247-1	Sequence 4, Appli
4	1212	99.3	289	14	US-10-280-679B-4	Sequence 4, Appli
5	1212	99.3	289	15	US-10-280-725B-4	Sequence 4, Appli
6	1209	99.0	247	14	US-10-277-890-6	Sequence 6, Appli
7	1209	99.0	247	17	US-10-717-243-5	Sequence 6, Appli
8	1071	87.7	247	9	US-09-192-793A-34	Sequence 34, Appli
9	1071	87.7	247	15	US-10-375-209A-34	Sequence 34, Appli
10	802	65.7	263	14	US-10-127-890-7	Sequence 7, Appli
11	802	65.7	263	17	US-10-717-243-7	Sequence 7, Appli
12	724.5	59.3	248	14	US-10-127-890-5	Sequence 5, Appli
13	724.5	59.3	248	17	US-10-717-243-5	Sequence 5, Appli

SEQUENCES

Result No.	Score	Query	Length	DB	ID	Description
1	1221	100.0	247	9	US-09-792-793A-39	Sequence 39, Appli
2	1221	100.0	247	15	US-10-375-209A-39	Sequence 39, Appli
3	1214	99.4	289	11	US-09-905-247-1	Sequence 4, Appli
4	1212	99.3	289	14	US-10-280-679B-4	Sequence 4, Appli
5	1212	99.3	289	15	US-10-280-725B-4	Sequence 4, Appli
6	1209	99.0	247	14	US-10-277-890-6	Sequence 6, Appli
7	1209	99.0	247	17	US-10-717-243-5	Sequence 6, Appli
8	1071	87.7	247	9	US-09-192-793A-34	Sequence 34, Appli
9	1071	87.7	247	15	US-10-375-209A-34	Sequence 34, Appli
10	802	65.7	263	14	US-10-127-890-7	Sequence 7, Appli
11	802	65.7	263	17	US-10-717-243-7	Sequence 7, Appli
12	724.5	59.3	248	14	US-10-127-890-5	Sequence 5, Appli
13	724.5	59.3	248	17	US-10-717-243-5	Sequence 5, Appli

SEQUENCES

Result No.	Score	Query	Length	DB	ID	Description
1	1221	100.0	247	9	US-09-792-793A-39	Sequence 39, Appli
2	1221	100.0	247	15	US-10-375-209A-39	Sequence 39, Appli
3	1214	99.4	289	11	US-09-905-247-1	Sequence 4, Appli
4	1212	99.3	289	14	US-10-280-679B-4	Sequence 4, Appli
5	1212	99.3	289	15	US-10-280-725B-4	Sequence 4, Appli
6	1209	99.0	247	14	US-10-277-890-6	Sequence 6, Appli
7	1209	99.0	247	17	US-10-717-243-5	Sequence 6, Appli
8	1071	87.7	247	9	US-09-192-793A-34	Sequence 34, Appli
9	1071	87.7	247	15	US-10-375-209A-34	Sequence 34, Appli
10	802	65.7	263	14	US-10-127-890-7	Sequence 7, Appli
11	802	65.7	263	17	US-10-717-243-7	Sequence 7, Appli
12	724.5	59.3	248	14	US-10-127-890-5	Sequence 5, Appli
13	724.5	59.3	248	17	US-10-717-243-5	Sequence 5, Appli

SEQUENCES

Result No.	Score	Query	Length	DB	ID	Description
1	1221	100.0	247	9	US-09-792-793A-39	Sequence 39, Appli
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3	1214	99.4	289	11	US-09-905-247-1	Sequence 4, Appli
4	1212	99.3	289	14	US-10-280-679B-4	Sequence 4, Appli
5	1212	99.3	289	15	US-10-280-725B-4	Sequence 4, Appli
6	1209	99.0	247	14	US-10-277-890-6	Sequence 6, Appli
7	1209	99.0	247	17	US-10-717-243-5	Sequence 6, Appli
8	1071	87.7	247	9	US-09-192-793A-34	Sequence 34, Appli
9	1071	87.7	247	15	US-10-375-209A-34	Sequence 34, Appli
10	802	65.7	263	14	US-10-127-890-7	Sequence 7, Appli
11	802	65.7	263	17	US-10-717-243-7	Sequence 7, Appli
12	724.5	59.3	248	14	US-10-127-890-5	Sequence 5, Appli
13	724.5	59.3	248	17	US-10-717-243-5	Sequence 5, Appli

SEQUENCES

Result No.	Score	Query	Length	DB	ID	Description
1	1221	100.0	247	9	US-09-792-793A-39	Sequence 39, Appli
2	1221	100.0	247	15	US-10-375-209A-39	Sequence 39, Appli
3	1214	99.4	289	11	US-09-905-247-1	Sequence 4, Appli
4	1212	99.3	289	14	US-10-280-679B-4	Sequence 4, Appli
5	1212	99.3	289	15	US-10-280-725B-4	Sequence 4, Appli
6	1209	99.0	247	14	US-10-277-890-6	Sequence 6, Appli
7	1209	99.0	247	17	US-10-717-243-5	Sequence 6, Appli
8	1071	87.7	247	9	US-09-192-793A-34	Sequence 34, Appli
9	1071	87.7	247	15	US-10-375-209A-34	Sequence 34, Appli
10	802	65.7	263	14	US-10-127-890-7	Sequence 7, Appli
11	802	65.7	263	17	US-10-717-243-7	Sequence 7, Appli
12	724.5	59.3	248	14	US-10-127-890-5	Sequence 5, Appli
13	724.5	59.3	248	17	US-10-717-243-5	Sequence 5, Appli

SEQUENCES

Result No.	Score	Query	Length	DB	ID	Description
1	1221	100.0	247	9	US-09-792-793A-39	Sequence 39, Appli
2	1221	100.0	247	15	US-10-375-209A-39	Sequence 39, Appli
3	1214	99.4	289	11	US-09-905-247-1	Sequence 4, Appli
4	1212	99.3	289	14	US-10-280-679B-4	Sequence 4, Appli
5	1212	99.3	289	15	US-10-280-725B-4	Sequence 4, Appli
6	1209	99.0	247	14	US-10-277-890-6	Sequence 6, Appli
7	1209	99.0	247	17	US-10-717-243-5	Sequence 6, Appli
8	1071	87.7	247	9	US-09-192-793A-34	Sequence 34, Appli
9	1071	87.7	247	15	US-10-375-209A-34	Sequence 34, Appli
10	802	65.7	263	14	US-10-127-890-7	Sequence 7, Appli
11	802	65.7	263	17	US-10-717-243-7	Sequence 7, Appli
12	724.5	59.3	248	14	US-10-127-890-5	Sequence 5, Appli
13	724.5	59.3	248	17	US-10-717-243-5	Sequence 5, Appli

SEQUENCES

Result No.	Score	Query	Length	DB	ID	Description
1	1221	100.0	247	9	US-09-792-793A-39	Sequence 39, Appli
2	1221	100.0	247	15	US-10-375-209A-39	Sequence 39, Appli
3	1214	99.4	289	11	US-09-905-247-1	Sequence 4, Appli
4	1212	99.3	289	14	US-10-280-679B-4	Sequence 4, Appli
5	1212	99.3	289	15	US-10-280-725B-4	Sequence 4, Appli
6	1209	99.0	247	14	US-10-277-890-6	Sequence 6, Appli
7	1209	99.0	247	17	US-10-717-243-5	Sequence 6, Appli
8	1071	87.7	247	9	US-09-192-793A-34	Sequence 34, Appli
9	1071	87.7	247	15	US-10-375-209A-34	Sequence 34, Appli
10	802	65.7	263	14	US-10-127-890-7	Sequence 7, Appli
11	802	65.7	263	17	US-10-717-243-7	Sequence 7, Appli
12	724.5	59.3	248	14	US-10-127-890-5	Sequence 5, Appli
13	724.5	59.3	248	17	US-10-717-243-5	Sequence 5, Appli

SEQUENCES

Result No.	Score	Query	Length	DB	ID	Description
1	1221	100.0	247	9	US-09-792-793A-39	Sequence 39, Appli
2	1221	100.0	247	15	US-10-375-209A-39	Sequence 39, Appli
3	1214	99.4	289	11	US-09-905-247-1	Sequence 4, Appli
4	1212	99.3	289	14	US-10-280-679B-4	Sequence 4, Appli
5	1212	99.3	289	15	US-10-280-725B-4	Sequence 4, Appli
6	1209	99.0	247	14	US-10-277-890-6	Sequence 6, Appli
7	1209	99.0	247	17	US-10-717-243-5	Sequence 6, Appli
8	1071	87.7	247	9	US-09-192-793A-34	Sequence 34, Appli
9	1071	87.7	247	15	US-10-375-209A-34	Sequence 34, Appli
10	802	65.7	263	14	US-10-127-890-7	Sequence 7, Appli
11	802	65.7	263	17	US-10-717-243-7	Sequence 7, Appli
12	724.5	59.3	248	14	US-10-127-890-5	Sequence 5, Appli
13	724.5	59.3	248	17	US-10-717-243-5	Sequence 5, Appli

SEQUENCES

Result No.	Score	Query	Length	DB	ID	Description
1	1221	100.0	247	9	US-09-792-793A-39	Sequence 39, Appli
2	1221	100.0	247	15	US-10-375-209A-39	Sequence 39, Appli
3	1214	99.4	289	11	US-09-905-247-1	Sequence 4, Appli
4	1212	99.3	289	14	US-10-280-679B-4	Sequence 4, Appli
5	1212	99.3	289	15	US-10-280-725B-4	Sequence 4, Appli
6	1209	99.0	247	14	US-10-277-890-6	Sequence 6, Appli
7	1209	99.0	247	17	US-10-717-243-5	Sequence 6, Appli
8	1071	87.7	247	9	US-09-192-793A-34	Sequence 34, Appli
9	1071	87.7	247	15	US-10-375-209A-34	Sequence 34, Appli
10	802	65.7	263	14	US-10-127-890-7	Sequence 7, Appli
11	802	65.7	263	17	US-10-717-243-7	Sequence 7, Appli
12	724.5	59.3	248	14	US-10-127-890-5	Sequence 5, Appli
13	724.5	59.3	248	17	US-10-717-243-5	Sequence 5, Appli

SEQUENCES

Result No.	Score	Query	Length	DB	ID	Description
1	1221	100.0	247	9	US-09-792-793A-39	Sequence 39, Appli
2	1221	100.0	247	15	US-10-375-209A-39	Sequence 39, Appli
3	1214	99.4	289	11	US-09-905-247-1	Sequence 4, Appli
4	1212	99.3	289	14	US-10-280-679B-4	Sequence 4, Appli
5	1212	99.3	289	15	US-10-280-725B-4	Sequence 4, Appli
6	1209	99.0	247	14	US-10-277-890-6	Sequence 6, Appli
7	1209	99.0	247	17	US-10-717-243-5	Sequence 6, Appli
8	1071	87.7	247	9	US-09-192-793A-34	Sequence 34, Appli
9	1071	87.7	247	15	US-10-375-209A-34	Sequence 34, Appli
10	802	65.7	263	14	US-10-127-890-7	Sequence 7, Appli
11	802	65.7	263	17	US-10-717-243-7	Sequence 7, Appli
12	724.5	59.3	248	14	US-10-127-890-5	Sequence 5, Appli
13	724.5	59.3	248	17	US-10-717-243-5	Sequence 5, Appli

SEQUENCES

Result No.	Score	Query	Length	DB	ID	Description
1	1221	100.0	247	9	US-09-792-793A-39	Sequence 39, Appli
2	1221	100.0	247	15	US-10-375-209A-39	Sequence 39, Appli
3	1214	99.4	289	11	US-09-905-247-1	Sequence 4, Appli
4	1212	99.3	289	14	US-10-280-679B-4	Sequence 4, Appli
5	1212	99.3	289	15	US-10-280-725B-4	Sequence 4, Appli
6	1209	99.0	247	14	US-10-277-890-6	Sequence 6, Appli

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RESULT 2
; US-10-375-209A-39
; Sequence 39, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601E
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 39
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Trichosanthus kirilowii
; US-10-375-209A-39

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Best Local Similarity 100.0%; Score 1221; DB 15; Length 247;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 DVSPRLSGATSSYGVFISNLKALPNEKLYDPLRSSLPSQSYALIHLTYADETI 60
Query 24 DVSPRLSGATSSYGVFISNLKALPNEKLYDPLRSSLPSQSYALIHLTYADETI 83
Db 24 DVSPRLSGATSSYGVFISNLKALPNEKLYDPLRSSLPSQSYALIHLTYADETI 83
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Db 144 SVAIDVNTYIMGRAGDTSYFNEASATEAKYVFKDAMRKVTLPSYENYRLQTAAGK 20
Query 84 SVAIDVNTYIMGRAGDTSYFNEASATEAKYVFKDAMRKVTLPSYENYRLQTAAGK 143
Db 84 SVAIDVNTYIMGRAGDTSYFNEASATEAKYVFKDAMRKVTLPSYENYRLQTAAGK 143
Query 121 IRENIPLGIPALDSAITLYVYNSAASALMVLQIOTSEARYKFIQOIGKVDKFL 180
Db 144 IRENIPLGIPALDSAITLYVYNSAASALMVLQIOTSEARYKFIQOIGKVDKFL 180
Query 181 PSLAISLENSWALSQKIQIASTNGQFESPVVLINAQNQRVTITNDAGVTSNIAL 240
Db 204 PSLAISLENSWALSQKIQIASTNGQFESPVVLINAQNQRVTITNDAGVTSNIAL 263
Query 241 LNRNIMA 247
Db 264 LNRNIMA 270

RESULT 3
; US-09-905-247-1
; Sequence 1, Application US/09905247
; Publication No. US20040197853A1
; GENERAL INFORMATION:
; APPLICANT: KE, TI-BAO
; APPLICANT: NIE, HUI-LING
; TITLER OF INVENTION: Mutant Trichosanthin
; FILE REFERENCE: 04399/000J615-US0
; CURRENT APPLICATION NUMBER: US/09/905,247
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: CN 00119553.0
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: CN 01103102.6
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO: 1
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Chinese cucumber protein alpha-trichosanthin
; US-10-375-209B-4

Query Match
Best Local Similarity 99.3%; Score 1212; DB 14; Length 289;
Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Query 1 DVSPRLSGATSSYGVFISNLKALPNEKLYDPLRSSLPSQSYALIHLTYADETI 60
Db 1 DVSPRLSGATSSYGVFISNLKALPNEKLYDPLRSSLPSQSYALIHLTYADETI 60
Query 24 DVSPRLSGATSSYGVFISNLKALPNEKLYDPLRSSLPSQSYALIHLTYADETI 83
Db 24 DVSPRLSGATSSYGVFISNLKALPNEKLYDPLRSSLPSQSYALIHLTYADETI 83
Query 61 SVAIDVNTYIMGRAGDTSYFNEASATEAKYVFKDAMRKVTLPSYENYRLQTAAGK 20
Db 144 SVAIDVNTYIMGRAGDTSYFNEASATEAKYVFKDAMRKVTLPSYENYRLQTAAGK 20
Query 84 SVAIDVNTYIMGRAGDTSYFNEASATEAKYVFKDAMRKVTLPSYENYRLQTAAGK 143
Db 84 SVAIDVNTYIMGRAGDTSYFNEASATEAKYVFKDAMRKVTLPSYENYRLQTAAGK 143
Query 121 IRENIPLGIPALDSAITLYVYNSAASALMVLQIOTSEARYKFIQOIGKVDKFL 180
Db 144 IRENIPLGIPALDSAITLYVYNSAASALMVLQIOTSEARYKFIQOIGKVDKFL 180
Query 181 PSLAISLENSWALSQKIQIASTNGQFESPVVLINAQNQRVTITNDAGVTSNIAL 240
Db 204 PSLAISLENSWALSQKIQIASTNGQFESPVVLINAQNQRVTITNDAGVTSNIAL 263
Query 241 LNRNIMA 247
Db 264 LNRNIMA 270

RESULT 4
; US-10-280-679B-4
; Sequence 4, Application US/10280679B
; Publication No. US20030150019A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
; FILE REFERENCE: LSBC-0108-US03
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 09/557, 941
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 08/484, 341
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/923, 692
; PRIOR FILING DATE: 1992-07-31
; PRIOR APPLICATION NUMBER: 07/600, 244
; PRIOR FILING DATE: 1990-10-22
; PRIOR APPLICATION NUMBER: 07/641, 617
; PRIOR FILING DATE: 1991-01-16
; PRIOR APPLICATION NUMBER: 07/737, 899
; PRIOR FILING DATE: 1991-07-26
; PRIOR APPLICATION NUMBER: 07/739, 143
; PRIOR FILING DATE: 1991-08-01
; PRIOR APPLICATION NUMBER: 07/310, 881
; PRIOR FILING DATE: 1989-02-17
; PRIOR APPLICATION NUMBER: 07/160, 766
; PRIOR FILING DATE: 1988-02-26
; PRIOR APPLICATION NUMBER: 07/160, 771
; PRIOR FILING DATE: 1988-02-25
; Remaining Prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Trichosanthes Kirilowii M.
; US-09-905-247-1

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RESULT 5
US-10-280-725B-4
; Sequence 4, Application US/10280-725B
; Publication No. US20040049025A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: Recombinant Viral Nucleic Acids
; FILE REFERENCE: LSGC-0109-US02
; CURRENT APPLICATION NUMBER: US/10/280,725B
; CURRENT FILING DATE: 2002-10-24
; PRIORITY APPLICATION NUMBER: 09/557,941
; PRIORITY FILING DATE: 2000-04-24
; PRIORITY APPLICATION NUMBER: 08/484,341
; PRIORITY FILING DATE: 1995-06-07
; PRIORITY APPLICATION NUMBER: 07/923,692
; PRIORITY FILING DATE: 1992-07-31
; PRIORITY APPLICATION NUMBER: 07/600,244
; PRIORITY FILING DATE: 1990-10-22
; PRIORITY APPLICATION NUMBER: 07/641,617
; PRIORITY FILING DATE: 1991-01-16
; PRIORITY APPLICATION NUMBER: 07/737,899
; PRIORITY FILING DATE: 1991-07-26
; PRIORITY APPLICATION NUMBER: 07/739,143
; PRIORITY FILING DATE: 1991-08-01
; PRIORITY APPLICATION NUMBER: 07/310,881
; PRIORITY FILING DATE: 1989-02-17
; PRIORITY APPLICATION NUMBER: 07/160,766
; PRIORITY FILING DATE: 1988-02-25
; PRIORITY APPLICATION NUMBER: 07/160,771
; PRIORITY FILING DATE: 1988-02-26
; Remaining Prior Application data removed - See file wrapper, or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Chinese cucumber
; US-10-280-725B-4

Query Match 99.3%; Score 1212; DB 15; Length 289;
Best Local Similarity 99.2%; Pred. No. 1.6e-11; Indels 0; Gaps 0;
Matches 245; Conservative 1; Mismatches 1;

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QY 24 DVSPRLSGATSSSYGVFISNLRKALPWERKLYDIPRLSSLPGSQRVALIHLTNYADBTI 83

QY 61 SVAIDVNTVNYIMGYRAGDTSYFNEEASATEAKVVKDAMRKVTLPSGYVERLQTAGK 120
QY 84 SVAIDVNTVNYIMGYRAGDTSYFNEEASATEAKVVKDAMRKVTLPSGYVERLQTAGK 143
QY 121 IRENIPGLPALSATITLYFVNANSASALMVLQISTSEARRYKFEQQIGKRVDKTFL 180
QY 144 IRENIPGLPALSATITLYFVNANSASALMVLQISTSEARRYKFEQQIGKRVDKTFL 203

Db 24 DVSPRLSGATSSSYGVFISNLRKALPWERKLYDIPRLSSLPGSQRVALIHLTNYADBTI 83
Db 61 SVAIDVNTVNYIMGYRAGDTSYFNEEASATEAKVVKDAMRKVTLPSGYVERLQTAGK 120
Db 84 SVAIDVNTVNYIMGYRAGDTSYFNEEASATEAKVVKDAMRKVTLPSGYVERLQTAGK 143

Db 121 IRENIPGLPALSATITLYFVNANSASALMVLQISTSEARRYKFEQQIGKRVDKTFL 180
Db 144 IRENIPGLPALSATITLYFVNANSASALMVLQISTSEARRYKFEQQIGKRVDKTFL 203

Db 241 LNRNNA 247
Db 264 LNRNNA 270

RESULT 6
US-10-127-890-6
; Sequence 6, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; CARROLL, Stephen F.
; STUDNICKA, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosomes-Inactivating Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Mandeville, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/646,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/701,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/987,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,913
; REFERENCE/DOCKET NUMBER: 200-70-P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amin acid
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
; US-10-127-890-6

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Best Local Similarity 99.2%; Pred. No. 2.6e-11; Indels 0; Gaps 0;
Matches 245; Conservative 0; Mismatches 2;

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QY 84 SVAIDVNTVNYIMGYRAGDTSYFNEEASATEAKVVKDAMRKVTLPSGYVERLQTAGK 143
QY 121 IRENIPGLPALSATITLYFVNANSASALMVLQISTSEARRYKFEQQIGKRVDKTFL 180

Db 144 IRENIPGLPALSATITLYFVNANSASALMVLQISTSEARRYKFEQQIGKRVDKTFL 203
QY 181 PSAIISLENSALSKOIQIASTNNQFESPVULINAQNQRTITNDAGUTSNIAALL 240
Db 204 PSAIISLENSALSKOIQIASTNNQFESPVULINAQNQRTITNDAGUTSNIAALL 263

Db 241 LNRNNA 247
Db 264 LNRNNA 270

1 DVSFRLSGATSSYGVFSNLRKALPNERKLYD; DVSFRSLPGSQRVALIHLTNYADETI 60
 QY ; SEQUENCE DESCRIPTION: SEQ ID NO: 6;
 61 SVAIDVNTVNYIMGYRAGDTSYFFNEASATEAKVYFKDAMRKVTPYSGNVERLQTAGK 120
 Db 61 SVAIDVNTVNYIMGYRAGDTSYFFNEASATEAKVYFKDAMRKVTPYSGNVERLQTAGK 120
 ; Best Local Similarity 99.0%; Score 1209; DB 17; Length 247;
 ; Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 121 IRENIPGLPLPALSATITLYFVNNSAASALMVLQIOTSEARRYKIEQIGRKDVKTEL 180
 Db 121 IRENIPGLPLPALSATITLYFVNNSAASALMVLQIOTSEARRYKIEQIGRKDVKTEL 180
 ; Query Match 99.0%; Score 1209; DB 17; Length 247;
 ; Best Local Similarity 99.2%; Pred. No. 2.6e-111;
 ; Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 181 PSLATISLENSWALSQKIQIASTNINGQFESPVLINAQNQRTITNDAGVTSNALL 240
 Db 181 PSLATISLENSWALSQKIQIASTNINGQFESPVLINAQNQRTITNDAGVTSNALL 240
 ; Query Match 99.0%; Score 1209; DB 17; Length 247;
 ; Best Local Similarity 99.2%; Pred. No. 2.6e-111;
 ; Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 181 PSLATISLENSWALSQKIQIASTNINGQFESPVLINAQNQRTITNDAGVTSNALL 240
 Db 181 PSLATISLENSWALSQKIQIASTNINGQFESPVLINAQNQRTITNDAGVTSNALL 240
 ; Query Match 99.0%; Score 1209; DB 17; Length 247;
 ; Best Local Similarity 99.2%; Pred. No. 2.6e-111;
 ; Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 241 LNRNNMA 247
 Db 241 LNRNNMA 247
 ; Query Match 99.0%; Score 1209; DB 17; Length 247;
 ; Best Local Similarity 99.2%; Pred. No. 2.6e-111;
 ; Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY RESULT 7
 US-10-717-243-6
 ; Sequence 6, Application US/10717243
 ; Publication No. US20050054835A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Batter, Marc D.
 ; CARROLL, Stephen F.
 ; STUDNIKA, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; NUMBER OF SEQUENCES: 169
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/717,243
 ; FILING DATE: 18-NOV-2003
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/839,765
 ; FILING DATE: 15-APR-1997
 ; APPLICATION NUMBER: US 08/425,336
 ; FILING DATE: 18-APR-1995
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-8889
 ; TELEFAX: 312/707-9155
 ; TELEX: 650 380-1248
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 247 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6;
 US-10-717-243-6
 ; Query Match 99.0%; Score 1209; DB 17; Length 247;
 ; Best Local Similarity 99.2%; Pred. No. 2.6e-111;
 ; Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DVSFRLSGATSSYGVFSNLRKALPNERKLYD; DVSFRSLPGSQRVALIHLTNYADETI 60
 Db 1 DVSFRLSGATSSYGVFSNLRKALPNERKLYD; DVSFRSLPGSQRVALIHLTNYADETI 60
 ; Query Match 99.0%; Score 1209; DB 17; Length 247;
 ; Best Local Similarity 99.2%; Pred. No. 2.6e-111;
 ; Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 61 SVAIDVNTVNYIMGYRAGDTSYFFNEASATEAKVYFKDAMRKVTPYSGNVERLQTAGK 120
 Db 61 SVAIDVNTVNYIMGYRAGDTSYFFNEASATEAKVYFKDAMRKVTPYSGNVERLQTAGK 120
 ; Query Match 99.0%; Score 1209; DB 17; Length 247;
 ; Best Local Similarity 99.2%; Pred. No. 2.6e-111;
 ; Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 121 IRENIPGLPLPALSATITLYFVNNSAASALMVLQIOTSEARRYKIEQIGRKDVKTEL 180
 Db 121 IRENIPGLPLPALSATITLYFVNNSAASALMVLQIOTSEARRYKIEQIGRKDVKTEL 180
 ; Query Match 99.0%; Score 1209; DB 17; Length 247;
 ; Best Local Similarity 99.2%; Pred. No. 2.6e-111;
 ; Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 181 PSLATISLENSWALSQKIQIASTNINGQFESPVLINAQNQRTITNDAGVTSNALL 240
 Db 181 PSLATISLENSWALSQKIQIASTNINGQFESPVLINAQNQRTITNDAGVTSNALL 240
 ; Query Match 99.0%; Score 1209; DB 17; Length 247;
 ; Best Local Similarity 99.2%; Pred. No. 2.6e-111;
 ; Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 181 PSLATISLENSWALSQKIQIASTNINGQFESPVLINAQNQRTITNDAGVTSNALL 240
 Db 181 PSLATISLENSWALSQKIQIASTNINGQFESPVLINAQNQRTITNDAGVTSNALL 240
 ; Query Match 99.0%; Score 1209; DB 17; Length 247;
 ; Best Local Similarity 99.2%; Pred. No. 2.6e-111;
 ; Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 241 LNRNNMA 247
 Db 241 LNRNNMA 247
 ; Query Match 99.0%; Score 1209; DB 17; Length 247;
 ; Best Local Similarity 99.2%; Pred. No. 2.6e-111;
 ; Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY RESULT 8
 US-09-792-793A-34
 ; Sequence 34, Application US/09792793A
 ; Patent No. US20020168370A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McDonald, John R.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AL
 ; FILE REFERENCE: 25020-601D
 ; CURRENT APPLICATION NUMBER: US/09/792,793A
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 93
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 34
 ; LENGTH: 247
 ; TYPE: PRT
 ; ORGANISM: Bryonia dioica
 ; US-09-792-793A-34
 ; Query Match 87.7%; Score 1071; DB 9; Length 247;
 ; Best Local Similarity 86.2%; Pred. No. 1.2e-97;
 ; Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DVSFRLSGATSSYGVFSNLRKALPNERKLYD; DVSFRSLPGSQRVALIHLTNYADETI 60
 Db 1 DVSFRLSGATSSYGVFSNLRKALPNERKLYD; DVSFRSLPGSQRVALIHLTNYADETI 60
 ; Query Match 87.7%; Score 1071; DB 9; Length 247;
 ; Best Local Similarity 86.2%; Pred. No. 1.2e-97;
 ; Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;
 QY 61 SVAIDVNTVNYIMGYRAGDTSYFFNEASATEAKVYFKDAMRKVTPYSGNVERLQTAGK 120
 Db 61 SVAIDVNTVNYIMGYRAGDTSYFFNEASATEAKVYFKDAMRKVTPYSGNVERLQTAGK 120
 ; Query Match 87.7%; Score 1071; DB 9; Length 247;
 ; Best Local Similarity 86.2%; Pred. No. 1.2e-97;
 ; Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;
 QY 121 IRENIPGLPLPALSATITLYFVNNSAASALMVLQIOTSEARRYKIEQIGRKDVKTEL 180
 Db 121 IRENIPGLPLPALSATITLYFVNNSAASALMVLQIOTSEARRYKIEQIGRKDVKTEL 180
 ; Query Match 87.7%; Score 1071; DB 9; Length 247;
 ; Best Local Similarity 86.2%; Pred. No. 1.2e-97;
 ; Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;
 QY 181 PSLATISLENSWALSQKIQIASTNINGQFESPVLINAQNQRTITNDAGVTSNALL 240
 Db 181 PSLATISLENSWALSQKIQIASTNINGQFESPVLINAQNQRTITNDAGVTSNALL 240
 ; Query Match 87.7%; Score 1071; DB 9; Length 247;
 ; Best Local Similarity 86.2%; Pred. No. 1.2e-97;
 ; Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

RESULT 9

US-10-375-209A-34
Sequence 34, Application US/10375209A

Publication No. US20030215421A1

GENERAL INFORMATION:

APPLICANT: McDonald, John R.

APPLICANT: Coggins, Philip

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND OTHER INFLAMMATORY CONDITIONS AND DISORDERS

FILE REFERENCE: 25020-601E

CURRENT APPLICATION NUMBER: US/10/375,209A

CURRENT FILING DATE: 2003-02-24

NUMBER OF SEQ ID NOS: 93

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 34

TYPE: PRT

ORGANISM: Bryonia dioica

US-10-375-209A-34

Query Match 87.7%; Score 1071; DB 15; Length 247;

Best Local Similarity 86.2%; Pred. No. 1.2e-97; Matches 213; Conservatve 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVSPRLSGATTTSYGVFISNLKALPVERKVDPLRSLSPSQRVALIHLNYADTTI 60
1 DVSPRLSGATTTSYGVFISNLKALPVERKVDPLRSLSPSQRVALIHLNYADTTI 60QY 61 SVAIDVNTVYIMGRAGDTSYFRENEASATEAKVVKPDKMRKVTLPSYNEMLQTAGK 120
61 SVAIDVNTVYIMGRAGDTSYFRENEASATEAKVVKPDKMRKVTLPSYNEMLQTAGK 120

Db 61 SVAIDVNTVYIMGRAGDTSYFRENEASATEAKVVKPDKMRKVTLPSYNEMLQTAGK 120

QY 121 IRENIPGLPALSATTTLYFVNANSAASALMVLQSTSEARVKFTRQIGRKRVDKTFL 180
121 IRENIPGLPALSATTTLYFVNANSAASALMVLQSTSEARVKFTRQIGRKRVDKTFL 180Db 181 PSLATISLENSWALSKOIQIOLQASTNGGOFESPVVLINAQNRQVITNDAGVTSNALL 240
181 PSLATISLENSWALSKOIQIOLQASTNGGOFESPVVLIDGNQRVSITNASARVVTNSNALL 240QY 241 LNRNMA 247
241 LNRNMA 247

Db 241 LNRNMA 247

RESULT 10
US-10-127-890-7
Sequence 7, Application US/10127890
Publication No. US20030166196A1

GENERAL INFORMATION:

APPLICANT: Batter, Marc D.

Carroll, Stephen F.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: IllinoisCOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994APPLICATION NUMBER: US 08/054,691
FILING DATE: 12-MAY-1993APPLICATION NUMBER: US 07/888,430
FILING DATE: 09-DEC-1992APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-127-890-7

Query Match 65.7%; Score 802; DB 14; Length 263;

Best Local Similarity 65.2%; Pred. No. 5.1e-71; Matches 161; Conservatve 37; Mismatches 49; Indels 0; Gaps 0;

QY 1 DVSPRLSGATTTSYGVFISNLKALPVERKVDPLRSLSPSQRVALIHLNYADTTI 60
1 DVSPRLSGATTTSYGVFISNLKALPVERKVDPLRSLSPSQRVALIHLNYADTTI 60Db 61 SVAIDVNTVYIMGRAGDTSYFRENEASATEAKVVKPDKMRKVTLPSYNEMLQTAGK 120
61 SVAIDVNTVYIMGRAGDTSYFRENEASATEAKVVKPDKMRKVTLPSYNEMLQTAGK 120QY 121 IRENIPGLPALSATTTLYFVNANSAASALMVLQSTSEARVKFTRQIGRKRVDKTFL 180
121 IRENIPGLPALSATTTLYFVNANSAASALMVLQSTSEARVKFTRQIGRKRVDKTFL 180Db 181 PSLATISLENSWALSKOIQIOLQASTNGGOFESPVVLINAQNRQVITNDAGVTSNALL 240
181 PSLATISLENSWALSKOIQIOLQASTNGGOFESPVVLIDGNQRVSITNASARVVTNSNALL 240QY 241 LNRNMA 247
241 LNRNMA 247

Db 241 LNRNMA 247

RESULT 11
US-10-717-243-7
Sequence 7, Application US/10717243
Publication No. US2005054835A1

GENERAL INFORMATION:

APPLICANT: Batter, Marc D.

Carroll, Stephen F.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 159

CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: IllinoisCOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US10/717,243

FILING DATE: 18-Nov-2003

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/839,765

FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

APPLICATION NUMBER: US/08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

SEQUENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-717-243-7

Query Match 65.7%; Score 802; DB 17; Length 263; Best Local Similarity 65.2%; Pred. No. 5.1e-71; Matches 161; Conservative 37; Mismatches 49; Indels 0; Gaps 0;

Qy 1 DVSPRLSGATSSYGVFISNLKALPNERKVDIPLRASSLPGSQRVALHILHNYADETI 60
1 DVSFRLSGADPRSYGMFPIKDLRNALPFRKEVNVIPULLPSVSGAGRVLHILHNYDGKTI 60Db 61 SVAIDVNVVYNGYRAGDTSYFVNEASATEAKYVFDAMKVTLPSPGNVYRQLQTAGK 120
61 TVAVDVNVVYNGYRAGDTSYFVNEASATEAKYVFDAMKVTLPSPGNVYRQLQTAGK 120Qy 61 TVAVDVNVVYNGYRAGDTSYFVNEASATEAKYVFDAMKVTLPSPGNVYRQLQTAGK 120
61 TVAVDVNVVYNGYRAGDTSYFVNEASATEAKYVFDAMKVTLPSPGNVYRQLQTAGK 120Db 121 IRENIPGGLPALSATIITFLYNTANSAASALMVLQIOTSEARRYKPEEQIGKRDVTFPL 180
121 IRENIPGGLPALSATIITFLYNTANSAASALMVLQIOTSEARRYKPEEQIGKRDVTFPL 180Qy 121 PREKIPGGLPALSATIITFLDSTAAMGALLVLIQTAEAKYRKPQQLQERAYDEV 180
121 PREKIPGGLPALSATIITFLDSTAAMGALLVLIQTAEAKYRKPQQLQERAYDEV 180Db 181 PSLAISLENSMSALKOIQIASTNNGQFESPVVLINAQNQRTITNDAGVTSNIAL 240
181 PSLAISLENSMSALKOIQIASTNNGQFESPVVLINAQNQRTITNDAGVTSNIAL 240Qy 181 PSLAISLENSMSALKOIQIASTNNGQFESPVVLINAQNQRTITNDAGVTSNIAL 240
181 PSLAISLENSMSALKOIQIASTNNGQFESPVVLINAQNQRTITNDAGVTSNIAL 240Db 241 LNRNNA 247
241 LNRNNA 247Db 241 LNRNNA 247
241 LNRNNA 247RESULT 12
US-10-127-890-5
; Sequence 5, Application US/10127890; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnicka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-APR-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

SEQUENCE/DOCKET NUMBER: 11022US09/200-70.P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 248 amino acids

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-127-890-5

Query Match 59.3%; Score 724.5; DB 14; Length 248; Best Local Similarity 59.0%; Pred. No. 2.7e-63; Matches 147; Conservative 49; Mismatches 50; Indels 3; Gaps 3;

Qy 1 DVSPRLSGATSSYGVFISNLKALPNERKVDIPLRASSLPGSQRVALHILHNYADETI 60
1 DVSFRLSGADPRSYGMFPIKDLRNALPFRKEVNVIPULLPSVSGAGRVLHILHNYDGKTI 60Db 61 IRENIPGGLPALSATIITFLYNTANSAASALMVLQIOTSEARRYKPEEQIGKRDVTFPL 180
121 IRENIPGGLPALSATIITFLYNTANSAASALMVLQIOTSEARRYKPEEQIGKRDVTFPL 180Qy 61 TVAVDVNVVYNGYRAGDTSYFVNEASATEAKYVFDAMKVTLPSPGNVYRQLQTAGK 120
121 IRENIPGGLPALSATIITFLDSTAAMGALLVLIQTAEAKYRKPQQLQERAYDEV 180Db 121 IRENIPGGLPALSATIITFLDSTAAMGALLVLIQTAEAKYRKPQQLQERAYDEV 180
121 IRENIPGGLPALSATIITFLDSTAAMGALLVLIQTAEAKYRKPQQLQERAYDEV 180Qy 121 PREKIPGGLPALSATIITFLDSTAAMGALLVLIQTAEAKYRKPQQLQERAYDEV 180
121 PREKIPGGLPALSATIITFLDSTAAMGALLVLIQTAEAKYRKPQQLQERAYDEV 180Db 181 PSLAISLENSMSALKOIQIASTNNGQFESPVVLINAQNQRTITNDAGVTSNIAL 240
181 PSLAISLENSMSALKOIQIASTNNGQFESPVVLINAQNQRTITNDAGVTSNIAL 240Qy 181 PSLAISLENSMSALKOIQIASTNNGQFESPVVLINAQNQRTITNDAGVTSNIAL 240
181 PSLAISLENSMSALKOIQIASTNNGQFESPVVLINAQNQRTITNDAGVTSNIAL 240Db 241 LNRNNA 247
241 LNRNNA 247Db 241 LNRNNA 247
241 LNRNNA 247RESULT 12
US-10-127-890-5
; Sequence 5, Application US/10127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; Carroll, Stephen F.

; Studnicka, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

RESULT 13
US-10-717-243-5
Sequence 5, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:

APPLICANT: Better, Marc D.

Carroll, Stephen F.

Studentka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/717,243

FILING DATE: 18-NOV-2003

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/839,765

FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 110222US09/200-70.P3.C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 249 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-717-243-5

Query Match 59.3%; Score 724.5; DB 17; Length 248;
Best Local Similarity 59.0%; Pred. No. 2.7e-63; Matches 147; Conservative 49; Mismatches 50; Indels 3; Gaps 3;

QY 1 DVSFRLSGATSSSYGVFTSNLRKALPNERKLYDPLRSPLPSQRVYALHILNTYADBTI 60

Db 1 DVSFRLSGATSSSYGVFTSNLRKALPNERKLYDPLRSPLPSQRVYALHILNTYADBTI 60

QY 61 SVAIDWNTNYIMGRADGYSYFENEASATEAAKVKPDKMVKYTLPSYGNVYELQTAKG 120

Db 61 TAVDVSOLYIMGYLNSTYFENESDAKASQVFKGS-TIVVLPYQGNVYELQTAKG 119

QY 121 IREMPILGLRALSATIYTYYNANSAASALMULQTSSEBARYKPIROQIGKVDKFL 180

Db 120 IREKPLGSPALDOSALTTFHYPOSTAAAFALVLOTAEASPKYIISQQLIRISKQY 179

RESULT 14
US-10-127-890-4
Sequence 4, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:

APPLICANT: Better, Marc D.

Carroll, Stephen F.

Studentka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/446,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/054,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/877,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 58.1%; Score 709; DB 14; Length 263;
Best Local Similarity 61.6%; Pred. No. 1e-61; Matches 149; Conservative 30; Mismatches 61; Indels 2; Gaps 2;

QY 1 DVSFRLSGATSSSYGVFTSNLRKALPNERKLYDPLRSPLPSQRVYALHILNTYADBTI 60

Db 1 DVSFRLSGATSSSYGVFTSNLRKALPNERKLYDPLRSPLPSQRVYALHILNTYADBTI 60

QY 61 SVAIDVNVVIMGYRAGDTSYFFNEASATEAKVVFKAQKUTLPYSGNVYERLQTAGK 120

Db 61 SVAIDVNVVYVAVTRVSYFFKE-SPEAVNLFK-GTRKITLPYTGNYENLQTAHK 118

QY 121 IRENIPGLPALSATITLFFYNAQSASALMVLQSTSEARYKFTBQQGKRVDKTF 180

Db 119 IRENIDGLPALSATITLFFYNAQSASALMVLQSTSEARYKFTBQQGKRVDKTF 178

QY 181 PSLATISLENSWALSKQIOLASTNINGQFESPVVLAQNYRQVITVNDAGVTSNALL 240

Db 179 PNLATISLENQNALSKQIFLAQNOCGKFRNPVDLIKPTGERQVNTNDSDVVKGNKLL 238

QY 241 LN 242

Db 239 LN 240

RESULT 15

US-10-717-243-4
; Sequence 4, Application US/10717243
; Publication No. US20050054835A1GENERAL INFORMATION:
APPLICANT: Better, Marc D.
CARROLL, Stephen F.
Studnitsa, Gary M.TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169 Proteins

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOSCURRENT APPLICATION DATA:
APPLICATION NUMBER: US10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/998,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/987,567
FILING DATE: 04-NOV-1991ATTORNEY/AGENT INFORMATION:
ATTORNEY NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-717-243-4

Query Match 58.1%; Score 709; DB 17; Length 263;

Best Local Similarity 61.6%; Pred. No. 1e-61; Indels 2; Gaps 2;

Matches 149; Conservative 30; Mismatches 61; Del 2;

Db 1 DVSFRISSGATSSSYGVFISNRKALPNERKLYDILRSLLPGSGRYALHLNTADETI 60

Db 1 DVNFDLSTATAKTYKIEDFRATLPFSHKYVDIPLYSTISDRFFLDTSYETI 60

QY 61 SVAIDVNVVIMGYRAGDTSYFFNEASATEAKVVFKAQKUTLPYSGNVYERLQTAGK 120

Db 61 SVAIDVNVVYVAVTRVSYFFKE-SPEAVNLFK-GTRKITLPYTGNYENLQTAHK 118

QY 181 PSLATISLENSWALSKQIOLASTNINGQFESPVVLAQNYRQVITVNDAGVTSNALL 240

Db 179 PNLATISLENQNALSKQIFLAQNOCGKFRNPVDLIKPTGERQVNTNDSDVVKGNKLL 238

QY 241 LN 242

Db 239 LN 240

Search completed: April 12, 2005, 15:31:53
Job time : 82.5633 Secs

RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=951433; Published=761907;
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
 RT "Studies on crystal structures, active-centre geometry and
 deproteinizing mechanism of two ribosome-inactivating proteins.";
 RL Biochem. J. 309:285-298(1995).
 CC -1- FUNCTION: Trichosanthin is an abortion-inducing protein. It is
 capable of inhibiting HIV-1 infection and replication. It
 inactivates eukaryotic 60S ribosomal subunits.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenine on the 28S rRNA.
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC Type 1 RIP subfamily.

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EMBL; M34858; AAA34207; 1; -.
 DR EMBL; J05434; AAA34206; 1; -.
 DR PIR; J0566; R1727.
 DR PDB; 1C1S; X-ray; A=23-270.
 DR PDB; 1G1U; X-ray; A=24-270.
 DR PDB; 1U4G; X-ray; A/B/C/D=23-270.
 DR PDB; 1MRJ; X-ray; @=24-270.
 DR PDB; 1MRK; X-ray; @=24-270.
 DR PDB; 1NLL; X-ray; A=23-270.
 DR PDB; 1O22; X-ray; A=24-270.
 DR PDB; 1RC5; X-ray; @=24-270.
 DR Interpro; IPR00174; RIP.
 DR PRINTS; PRO0396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW 3D-structure; Antiviral; Direct protein sequencing; Hydrolase;
 KW Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 23
 FT CHAIN 24 270
 PROPEP Ribosome-inactivating protein alpha-
 PROPEP trichosanthin.
 FT ACT SITE 271 289
 FT Removed in mature form.
 FT CONFLICT 183 183
 FT BY similarity.
 FT CONFLICT 57 60
 FT IPLI -> DPPI (in Ref. 4).
 FT CONFLICT 82 84
 FT Missing (in Ref. 4).
 FT CONFLICT 87 87
 FT I -> L (in Ref. 4).
 FT V -> VDAQIPRRAVL (in Ref. 4).
 FT CONFLICT 92 92
 FT KI -> GL (in Ref. 4).
 FT CONFLICT 143 144
 FT K -> S (in Ref. 4).
 FT CONFLICT 196 196
 FT MS -> LML (in Ref. 4).
 FT CONFLICT 215 216
 FT Q -> T (in Ref. 4).
 FT CONFLICT 231 231
 FT S -> T (in Ref. 2).
 FT CONFLICT 234 234
 FT S -> T (in Ref. 2).
 FT CONFLICT 246 246
 FT Missing (in Ref. 4).
 FT CONFLICT 247 247
 FT T -> M (in Ref. 2).
 STRAND 25 28
 TURN 30 31
 HELIX 34 46
 TURN 47 47
 STRAND 50 54
 TURN 55 56
 STRAND 57 60
 HELIX 66 69
 STRAND 70 76
 TURN 78 79
 STRAND 82 88
 TURN 89 92
 STRAND 93 99
 TURN 100 101
 STRAND 102 105
 HELIX 109 114
 TURN 115 117
 TURN 120 121

FT STRAND 124 127
 FT HELIX 134 141
 FT TURN 142 142
 FT HELIX 145 147
 FT STRAND 150 150
 FT HELIX 152 163
 FT TURN 164 165
 FT HELIX 167 180
 FT TURN 181 181
 FT HELIX 182 186
 FT STRAND 187 187
 FT HELIX 188 195
 FT TURN 196 196
 FT STRAND 202 202
 FT HELIX 206 226
 FT TURN 227 230
 FT STRAND 231 239
 FT TURN 241 242
 FT STRAND 245 250
 FT TURN 251 252
 FT HELIX 254 258
 FT TURN 259 259
 FT STRAND 260 260
 FT STRAND 263 263
 FT TURN 266 268
 FT STRAND 289 AA; 31676 MW; 5CE09BB630575BB9 CRC64;
 SQ SEQUENCE 289
 Query Match 100 %; Score 1221; DB 1; Length 289;
 Best Local Similarity 100 %; Pred No. 4; 78-92; Mismatches 0; Indels 0; Gaps 0;
 Matches 247; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 Qy 1 DVSFRLSGATSSYGVTFISNLRKALPNERKLYDIPRLSSLPGSORYALHLTYADETI 60
 Db 84 SVAIDVTVVYINGYRADTSFFNEASATEAKYFKDAMRKVTLIPYSQGIVERLQTAGK 143
 Qy 24 DVSFRLSGATSSYGVTFISNLRKALPNERKLYDIPRLSSLPGSORYALHLTYADETI 83
 Qy 61 SVAIDVTVVYINGYRADTSFFNEASATEAKYFKDAMRKVTLIPYSQGIVERLQTAGK 120
 Db 84 SVAIDVTVVYINGYRADTSFFNEASATEAKYFKDAMRKVTLIPYSQGIVERLQTAGK 143
 Qy 121 IRENTPIGLPAIDSATTLFYNNANASASALMVIQTSSEARYKPIEQQIGKRVDTKFL 180
 Db 144 IRENTPIGLPAIDSATTLFYNNANASASALMVIQTSSEARYKPIEQQIGKRVDTKFL 203
 Qy 181 PSALAISSLENSWALSQKIQIASTNGQFESPVUINAQNORVITTNVDAVGWTNIAL 240
 Db 204 PSALAISSLENSWALSQKIQIASTNGQFESPVUINAQNORVITTNVDAVGWTNIAL 263
 Qy 241 LNRNNMA 247
 Db 264 LNRNNMA 270

RESULT 2

ID Q84SVB PRELIMINARY; PRT; 289 AA.

AC 084SVB;
 DR 01-JUN-2003 (T-EMBLrel. 24, Created)
 DR 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DR 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Trichosanthin.

GN Name=PCs;
 OC Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yuan H., Wang L., Liu T., An C., Chen Z.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenine on the 28S rRNA.
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.

	FT SIGNAL 1	23	Potential.
	FT CHAIN 24	270	trichosanthin.
SQ	SEQUENCE 289 AA;	31706 MW;	A6D5602549CA5657 CRC64;
Query Match	99.8%; Score 1218; DB 2; Length 289;		
Best Local Similarity	99.6%; Pred. No. 8; 3e-92;		
Matches	246; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
QY	1 DVSPRLSGATSSSYGVFISNLRKALPWERKLKDPLRSLPSQRYALIHLTNYADBTI 60	QY	1 DVSPRLSGATSSSYGVFISNLRKALPWERKLKDPLRSLPSQRYALIHLTNYADBTI 60
Db	24 DVSPRLSGATSSSYGVFISNLRKALPWERKLKDPLRSLPSQRYALIHLTNYADBTI 83	Db	24 DVSPRLSGATSSSYGVFISNLRKALPWERKLKDPLRSLPSQRYALIHLTNYADBTI 83
QY	61 SVAIDVTNTVIMGYRAGDTSYFNFNEASATEAKVVFORKMVKYTLPSQGYNYERLQTAGK 120	QY	61 SVAIDVTNTVIMGYRAGDTSYFNFNEASATEAKVVFORKMVKYTLPSQGYNYERLQTAGK 120
Db	84 SVAIDVTNTVIMGYRAGDTSYFNFNEASATEAKVVFORKMVKYTLPSQGYNYERLQTAGK 143	Db	84 SVAIDVTNTVIMGYRAGDTSYFNFNEASATEAKVVFORKMVKYTLPSQGYNYERLQTAGK 143
QY	121 IRENIPGLPALSATITLYFVNANSASALMVIQTSSEARYKFIQOIGKRDVKFL 180	QY	121 IRENIPGLPALSATITLYFVNANSASALMVIQTSSEARYKFIQOIGKRDVKFL 180
Db	144 IRENIPGLPALSATITLYFVNANSASALMVIQTSSEARYKFIQOIGKRDVKFL 203	Db	144 IRENIPGLPALSATITLYFVNANSASALMVIQTSSEARYKFIQOIGKRDVKFL 203
QY	181 PSIAIISLENSWALSALKOIQIQAESTNNQFESPVVLINAQNQRVITNDAGVTSNALL 240	QY	181 PSIAIISLENSWALSALKOIQIQAESTNNQFESPVVLINAQNQRVITNDAGVTSNALL 240
Db	204 PSIAIISLENSWALSALKOIQIQAESTNNQFESPVVLINAQNQRVITNDAGVTSNALL 263	Db	204 PSIAIISLENSWALSALKOIQIQAESTNNQFESPVVLINAQNQRVITNDAGVTSNALL 263
QY	241 LNRNNA 247	QY	241 LNRNNA 247
Db	264 LNRNNA 270	Db	264 LNRNNA 270
RESULT 3			
O94KE4	PRELIMINARY; PRT; 289 AA.	O41216	PRELIMINARY; PRT; 289 AA.
AC	O94KE4; 01-DEC-2001 (TREMBLrel. 19, Created)	AC	O41216; 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Trichosanthin precursor.	DE	Trichosanthin.
GN	Name=TCS; OS Trichosanthes kirilowii (Mongolian snake-gourd).	GN	Name=trichosanthin; Synonyms=TCS;
OS	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucommiae; Cucurbitales; Cucurbitaceae; Trichosanthes.	OS	Trichosanthes kirilowii (Mongolian snake-gourd).
OC		OC	
OC		OC	
CC		CC	
CC		CC	
OX		OX	
NCBI_TAXID=3677;	[1]	NCBI_TAXID=3677;	
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RX	MEDLINE:94271613; PubMed=8003348;	RX	MEDLINE:94271613; PubMed=8003348;
RA	Zheng H., Wang B., Shaw P., Yeung H.; I Chuan Hsueh Pao 21:42-51(1994).	RA	Zheng H., Wang B., Shaw P., Yeung H.; I Chuan Hsueh Pao 21:42-51(1994).
RT	Cloning and DNA sequencing of the gene encoding trichosanthin.;	RT	Cloning and DNA sequencing of the gene encoding trichosanthin.;
RL	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one	RL	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC	specific adenosine on the 28S rRNA.	CC	specific adenosine on the 28S rRNA.
CC	-1- SIMILARITY: Belongs to the ribosome-inactivating protein family.	CC	-1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR	EMBL; S70176; AB31048.1; -.	DR	EMBL; S70176; AB31048.1; -.
DR	PIR; JC5032; JC5032.	DR	PIR; JC5032; JC5032.
DR	RESP; P09989; 1M4G.	DR	GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
DR	GO; GO:0016787; F:Hydrolyase activity; IEA.	DR	GO; GO:001748; P:negative regulation of protein biosynthesis; IEA.
DR	GO; GO:000592; P:defense response; IEA.	DR	InterPro; IPR001574; RIP.
DR	GO; GO:000652; P:defense response; IEA.	DR	Pfam; PF00161; RIP; 1.
DR	GO; GO:001748; P:negative regulation of protein biosynthesis; IEA.	DR	PRINTS; PR00396; SHIGARICIN.
DR	GO; GO:0009405; P:Pathogenesis; IEA.	DR	PRINTS; PR00275; SHIGARICIN.
DR	InterPro; IPR001574; RIP.	DR	Hydrolyase; Plant defense; Protein synthesis inhibitor; Toxin.
DR	PRINTS; PR00396; SHIGARICIN.	DR	Hydrolyase; Plant defense; Protein synthesis inhibitor; Toxin.
KW	Hydrolyase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.	KW	Hydrolyase; Plant defense; Protein synthesis inhibitor; Toxin.
QY	1 DVSPRLSGATSSSYGVFISNLRKALPWERKLKDPLRSLPSQRYALIHLTNYADBTI 60	QY	1 DVSPRLSGATSSSYGVFISNLRKALPWERKLKDPLRSLPSQRYALIHLTNYADBTI 60
Db	24 DVSPRLSGATSSSYGVFISNLRKALPWERKLKDPLRSLPSQRYALIHLTNYADBTI 83	Db	24 DVSPRLSGATSSSYGVFISNLRKALPWERKLKDPLRSLPSQRYALIHLTNYADBTI 83
QY	61 SVAIDVTNTVIMGYRAGDTSYFNFNEASATEAKVVFORKMVKYTLPSQGYNYERLQTAGK 120	QY	61 SVAIDVTNTVIMGYRAGDTSYFNFNEASATEAKVVFORKMVKYTLPSQGYNYERLQTAGK 120

Db 84 SVAVDVTIVVYIMGRAGDTISYFNEASATEAKVFKDMRKVTLPISGNRYLQLTAGK 143
 Qy 121 IRENIPGLPGLPALSATIITLYYVANSAASALMQLIQSTSEAAKYFEOQGKRVDKTFL 180
 Db 144 IRENIPGLPGLPALSATIITLYYVANSAASALMQLIQSTSEAAKYFEOQGKRVDKTFL 203
 Qy 181 PSLAISLENSWALSQKIQIYSTNGQFESPVULINAQNQRTITNDAGUTSNALL 240
 Db 204 PSLAISLENSWALSQKIQIYSTNGQFESPVULINAQNQRTITNDAGUTSNALL 263
 Qy 241 LNRNNA 247
 Db 264 LNRNNA 270

RESULT 5
 Q6BBQ4 PRELIMINARY; PRT; 247 AA.
 AC 06BBQ4;
 DT 25-OCT-2004 (Tremblel. 28, Created)
 DT 25-OCT-2004 (Tremblel. 28, Last sequence update)
 DE Trichosanthin (Fragnant).
 GN Name=TGS;
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mi S.-L.; Wang Y.-Y.; Li Y.-Y.; Chen Z.-L.; An C.-C.;
 RT "Trichosanthes kirilowii trichosanthin (TGS) mature peptide gene.";
 RL Submitted (JUN-2004) to the JUN/GenBank/DBJ database.
 CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenose on the 28S rRNA.
 CC -I- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 EMBL; A16981; ART9190.1; -.
 DR GO: GO-001748; F: rRNA N-glycosylase activity; IEA.
 DR InterPro; IPR01574; RIP.
 DR PRINTS; PF00161; RIP; 1.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 DR Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
 FT NON_TER 1 1
 FT CHAIN <1 247
 FT NON_TER 247 247
 SQ SEQUENCE 247 AA; 27172 MW; BCB:62884:P89CCB CRC64;

Query Match 97.9%; Score 1195; DB 2; Length 247;
 Best Local Similarity 97.6%; Pred. No. 5.2e-90;
 Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DVSFRLSGATSSYGVFISNLKALPNERKLYDPLRSLSLPGSQRVALHTNADETI 60
 Db 1 DVSFRLSGATSSYGVFISNLKALPNERKLYDPLRSLSLPGSQRVALHTNADETI 60
 Qy 61 SVAIDVTVVYIMGRAGDTISYFNEASATEAKVFKDMRKVTLPISGNRYLQLTAGK 120
 Db 61 SVAIDVTVVYIMGRAGDTISYFNEASATEAKVFKDMRKVTLPISGNRYLQLTAGK 120
 Qy 121 IRENIPGLPGLPALSATIITLYYVANSAASALMQLIQSTSEAAKYFEOQGKRVDKTFL 180
 Db 121 IRENIPGLPGLPALSATIITLYYVANSAASALMQLIQSTSEAAKYFEOQGKRVDKTFL 180
 Qy 181 PSLAISLENSWALSQKIQIYSTNGQFESPVULINAQNQRTITNDAGUTSNALL 240
 Db 181 PSLAISLENSWALSQKIQIYSTNGQFESPVULINAQNQRTITNDAGUTSNALL 240
 Qy 241 LNRNNA 247

RESULT 6
 RIPS_TRIKI STANDARD; PRT; 289 AA.
 AC P24478;
 DR 01-MAR-1992 (Rel. 21, Created)
 DR 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Ribosome-inactivating protein karsurin precursor (EC 3.2.2.22) (rRNA N-glycosidase).
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Root tuber;
 RX MEDLINS=97356522; PubMed=9212998;
 RL Mizukami H.; Toda K.; Kondo T.; Ogihara Y.;
 CC "Cloning and bacterial expression of a gene encoding ribosome-inactivating protein, karsurin-A and karsurin-C, from Trichosanthes
 RT karsurin var. Japonica"; Takeda T.; Kato Y.; Wakabayashi K.; Ogihara Y.;
 RN Biol. Pharm. Bull. 20:711-713 (1997).
 DR SEQUENCE OF 24-270.
 MEDLINE=92005931; PubMed=1914000;
 RA Toyokawa S.; Takeda T.; Kato Y.; Wakabayashi K.; Ogihara Y.;
 RT "The complete amino acid sequence of an abortifacient protein, karsurin.";
 RL Chem. Pharm. Bull. 39:1244-1249 (1991).
 CC -I- FUNCTION: Abortion-inducing protein. It inactivates eukaryotic 60S
 CC ribosomal subunits.
 CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenose on the 28S rRNA.
 CC -I- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC -I- SIMILARITY: Type I RIP subfamily.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB000666; BAA21786.1; -.
 DR PIR; JCB506; JCB5606.
 DR PIR; JU0393; JU0393.
 DR HSSP; P0989; IMRJ.
 DR InterPro; IPR01574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PRO0396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 DR Antiviral; Direct protein sequencing; Hydrolase; Plant defense;
 KW Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 21
 FT CHAIN 22 270
 FT C. Ribosome-inactivating protein karsurin-
 FT CHAIN 24 270
 FT A. Removed in mature form.
 FT PROPEP 271 289
 FT ACT SITE 183 183
 FT SEQUENCE 289 AA; 31704 MW; 883D3E34288B26 CRC64;
 SQ

Query Match 97.9%; Score 1194; DB 1; Length 289;
 Best Local Similarity 97.6%; Pred. No. 7.7e-90;
 Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db	24 DVSRFLSGATSSSYGVFISNLRKALPVERKLYDIPLRSLTLPGSQRVALIHLTNAYBETI	83	Db	121 IRENIPGLPALSATITLYFVNANSASALMWLIQTSSEARYKFEQQIGKRVDKTFI	180
Qy	61 SVAIDVTNYYIMGYRAGDTSYFNEASATEAKVVFCDAMRKVTLPLPSGNYERLQTAGK	120	Qy	181 PSAIISLENSWALSALKOIQIASTNGQFESPVLINAONQRTITNDAGVTSNALL	240
Db	84 SVAIDVTNYYVMGYRAGDTSYFNEASATEAKVVFCDAMRKVTLPLPSGNYERLQTAGK	143	Db	181 PSAIISLENSWALSALKOIQIASTNGQFESPVLINAONQRTITNDAGVTSNALL	240
Qy	121 IRENIPGLPALSATITLYFVNANSASALMWLIQTSSEARYKFEQQIGKRVDKTFI	180	Qy	241 LNRNNA 247	
Db	144 IRENIPGLPALSATITLYFVNANSASALMWLIQTSSEARYKFEQQIGKRVDKTFI	203	Db	241 PNRNNA 247	
Qy	181 PSAIISLENSWALSALKOIQIASTNGQFESPVLINAONQRTITNDAGVTSNALL	240			
Db	204 PSAIISLENSWALSALKOIQIASTNGQFESPVLINAONQRTITNDAGVTSNALL	263			
Qy	241 LNRNNA 247				
Db	264 LNRNNA 270				
RESULT 7					
Q9LRE3	PRELIMINARY;	PRT;	247 AA.		
ID	Q9LRE3				
AC	Q9LRE3;				
DT	01-OCT-2000 (TREMBLrel. 15, Created)				
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)				
DB	Trichobakin (Fragment).				
GN	Name=TBK;				
OS	Trichobanthes sp. Bac Kan 8-98.				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; rosids; eurosid I; Cucurbitales; Cucurbitaceae; Trichosanthes.				
OC	euroides I; Cucurbitales; Cucurbitaceae; Trichosanthes.				
NCBI_TaxID=18182;					
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21476888; PubMed=11592913;				
RA	Van Chi P., Quoc Truong H., Thuy Ha N., Chung W.I., Binh L.T.;				
RT	"Characterization of trichobakin, a type I ribosome-inactivating protein from Trichosanthes sp. Bac Kan 8-98.,"				
RL	Biotechnol. Appl. Biochem. 34:85-92(2001)				
CC	-I CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenine on the 28S rRNA.				
CC	-- SIMILARITY: Belongs to the ribosome-inactivating protein family.				
DR	EMBL: AB039324; BAA92530.1; -.				
DR	P09989; JUGG.				
DR	Q0_0016787; F:Hydrolase activity; IEA.				
DR	Q0_0030598; F:RNA N-glycosylase activity; IEA.				
DR	Q0_000952; P:Defense response; IEA.				
DR	Q0_0011748; P:negative regulation of protein biosynthesis; IEA.				
DR	Q0_0009405; P:Pathogenesis; IEA.				
DR	InterPro: IPR01574; RIP.				
DR	InterPro: IPR00161; RIP; I.				
DR	PRINTS; PR00396; SHIGARICIN.				
DR	PROSITE; PR00375; SHIGARICIN.				
DR	KW Hydrobase; Plant defense; Protein synthesis inhibitor; Toxin.				
FT	Hydrobase; Plant defense; Protein synthesis inhibitor; Toxin.				
FT	NON_TER 1				
FT	247 247 AA; 27199 MW;				
FT	SEQUENCE 247 AA; 270 AA; 29993 MW; 3D73FB461EA8E804 CRC64;				
Qy	Query Match 95.2%; Score 1162; DB 2; Length 270; Best Local Similarity 94.7%; Pred. No. 3e-87; 7; Indels 0; Gaps 0; Matches 234; Conservative 6; Mismatches 7; Indels 0; Gaps 0;				
Db	1 DVSRFLSGATSSSYGVFISNLRKALPVERKLYDIPLRSLTLPGSQRVALIHLTNAYBETI	60	Qy	61 SVAIDVTNYYIMGYRAGDTSYFNEASATEAKVVFCDAMRKVTLPLPSGNYERLQTAGK	120
Db	84 SVAIDVTNYYVMGYRAGDTSYFNEASATEAKVVFCDAMRKVTLPLPSGNYERLQTAGK	143	Db	84 SVAIDVTNYYIMGYRAGDTSYFNEASATEAKVVFCDAMRKVTLPLPSGNYERLQTAGK	143
Qy	1 DVSRFLSGATSSSYGVFISNLRKALPVERKLYDIPLRSLTLPGSQRVALIHLTNAYBETI	60	Qy	121 IRENIPGLPALSATITLYFVNANSASALMWLIQTSSEARYKFEQQIGKRVDKTFI	180
Db	1 DVSRFLSGATSSSYGVFISNLRKALPVERKLYDIPLRSLTLPGSQRVALIHLTNAYBETI	60	Qy	144 IRENIPGLPALSATITLYFVNANSASALMWLIQTSSEARYKFEQQIGKRVDKTFI	203
Qy	61 SVAIDVTNYYIMGYRAGDTSYFNEASATEAKVVFCDAMRKVTLPLPSGNYERLQTAGK	120	Qy	181 PSAIISLENSWALSALKOIQIASTNGQFESPVLINAONQRTITNDAGVTSNALL	240
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Qy	121 IRENIPGLPALSATITLYFVNANSASALMWLIQTSSEARYKFEQQIGKRVDKTFI	180	Qy	241 LNRNNA 247	

Search completed: April 12, 2005, 15:13:59
Job time : 107.91 sec

Qy 181 PSIAATISLENSWALSALKOIQIASTNNGQFESPVULINAQNQRTITVDAWVTSNALL 240
202 PSPAALSLLENSWALSALKOIQIASTNNGAFRTPVVITNDKGQRVEIKDVNSKVNINIKL 261
Qy 241 LN>NNMA 247
Db 262 LNQNTIA 268

RESULT 15

0684J5 PRELIMINARY; PPT; 264 AA.

AC Q684J5; 0684J5;

DT 25-OCT-2004 (TREMBLrel. 28, Created)

DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)

DE Type I ribosome inactivating protein precursor (Fragment).

GN Name=RIP;

OS Momordica charantia (Bitter gourd) (Balsam pear).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermato phyta; Magnoliophyta; eudicots; core eudicots; rosids;

OC eurosids I; Cucurbitales; Cucurbitaceae; Momordica.

OX NCBI_TaxID:3673;

RN [1]

RP SBQUENCE FROM N.A.

RA Nguyen Dinh C., Nguyen Thuy D., Le Thi Thu H., Nguyen Huy H.,

RA Tran Thi Phuong L., Nong Van H.;

RT "Expression of a gene encoding ribosome inactivating protein from

RT bitter melon (Momordica charantia).";

RT Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SBQUENCE FROM N.A.

RA Nong V.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

RL CC -1 CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one

CC specific adenosine on the 28S rRNA.

CC -1 SIMILARITY: Belongs to the ribosome-inactivating protein family.

DR EMBL: AJ748278; CAH19208.1; -.

DR InterPro: IPR01574; RIP.

DR PRAM: PF00161; RIP; 1.

DR PROSITE: PRO0396; SHIGARICIN.

DR KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.

FT NON_TER 1 1 Potential.

FT SIGNAL <1 1

FT CHAIN 2 264 type I ribosome inactivating protein.

SQ SEQUENCE 264 AA; 29775 MW; AD9E1175B0521AD CRC64;

Query Match Best Local Similarity 58.2%; Score 711; DB 2; Length 264;

Matches 149; Conservative 31; Mismatches 60; Indels 2; Gaps 2;

Qy 1 DVSPRLSGATSSYGVFISNLKALPWERKVDIPRLSSPGSQRVALIHLTNAYETI 60

Db 2 DVNFDLSTATAKTYKTFEDFRATLPFSHKVVDIPLYSTSDSRFLNLLNTSYAVTI 61

Qy 61 SVAIDVTVWVYMOYRAGDTSYFNEASATEAKVVKDAMRKVLPVSGNVRLLQTAAGK 120

Db 62 SVAIDVTVWVWYAWTRDVSYFKE-SPEEATNLFK-GTRKILTPYTGNTENLQTAHK 119

Qy 121 IRENIPGGLPALSATIITFYNNNSAASALAMVLIQSTSEAAKYKFEQOQGRVDTFL 180

Db 120 IRENIDGGLPALSATIITFYNNNSAASALAMVLIQSTSEAAKYKFEQOQGRVDTFL 179

Qy 181 PSIAATISLENSWALSALKOIQIASTNNGQFESPVULINAQNQRTITVDAWVTSNALL 240

Db 180 PSIAATISLENSWALSALKOIQIASTNNGQFESPVULINAQNQRTITVDAWVTSNALL 239

Qy 241 LN 242

Db 240 LN 241

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: April 12, 2005, 15:14:19 ; Search time 95.4347 Seconds

(without alignments) 1005.370 Million cell updates/sec

Title: US-09-905-247a-1

Perfect score: 1431

Sequence: 1 MIRFLVLSLILTLFLTTPA.....AAMDDDPVPTQSGCGSYAL 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications DB:*

1: /cggn2_6/ptocat/a/1/pubpaal/US07_PUBCOMB.pep:*

2: /cggn2_6/ptocat/a/1/pubpaal/PCT_NEW_PUB.pep:*

3: /cggn2_6/ptocat/a/1/pubpaal/US06_NEW_PUB.pep:*

4: /cggn2_6/ptocat/a/1/pubpaal/US07_NEW_PUB.pep:*

5: /cggn2_6/ptocat/a/1/pubpaal/US07_NEW_PUB.pep:*

6: /cggn2_6/ptocat/a/1/pubpaal/PTCT9_PUBCOMB.pep:*

7: /cggn2_6/ptocat/a/1/pubpaal/US08_NEW_PUB.pep:*

8: /cggn2_6/ptocat/a/1/pubpaal/US08_PUBCOMB.pep:*

9: /cggn2_6/ptocat/a/1/pubpaal/US09_PUBCOMB.pep:*

10: /cggn2_6/ptocat/a/1/pubpaal/US09_PUBCOMB.pep:*

11: /cggn2_6/ptocat/a/1/pubpaal/US09C_PUBCOMB.pep:*

12: /cggn2_6/ptocat/a/1/pubpaal/US09C_PUBCOMB.pep:*

13: /cggn2_6/ptocat/a/1/pubpaal/US09C_PUBCOMB.pep:*

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16: /cggn2_6/ptocat/a/1/pubpaal/US10D_PUBCOMB.pep:*

17: /cggn2_6/ptocat/a/1/pubpaal/US10 NEW_PUB.pep:*

18: /cggn2_6/ptocat/a/1/pubpaal/US11_NEW_PUB.pep:*

19: /cggn2_6/ptocat/a/1/pubpaal/US60_NEW_PUB.pep:*

20: /cggn2_6/ptocat/a/1/pubpaal/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

14 709 49.5 263 14 US-10-127-890-4 Sequence 4, Appli
 15 709 49.5 263 17 US-10-717-243-4 Sequence 4, Appli
 16 421 29.4 267 14 US-10-282-935-1 Sequence 1, Appli
 17 421 29.4 267 14 US-10-127-890-1 Sequence 1, Appli
 18 421 29.4 267 15 US-10-440-796-1 Sequence 1, Appli
 19 421 29.4 267 17 US-10-717-243-1 Sequence 1, Appli
 20 421 29.4 267 14 US-10-083-336A-1 Sequence 1, Appli
 21 342 23.9 198 14 US-10-083-336A-3 Sequence 3, Appli
 22 342 23.9 198 14 US-10-083-336A-7 Sequence 7, Appli
 23 342 23.9 199 14 US-10-083-336A-5 Sequence 5, Appli
 24 342 23.9 200 14 US-10-083-336A-10 Sequence 10, Appli
 25 337.5 23.6 185 14 US-10-083-336A-9 Sequence 9, Appli
 26 336 23.5 188 14 US-10-083-336A-4 Sequence 4, Appli
 27 336 23.5 189 14 US-10-083-336A-8 Sequence 8, Appli
 28 336 23.5 190 14 US-10-083-336A-6 Sequence 6, Appli
 29 336 23.5 190 14 US-10-083-336A-11 Sequence 11, Appli
 30 330 23.1 251 14 US-10-282-935-3 Sequence 3, Appli
 31 330 23.1 251 15 US-10-440-796-3 Sequence 9, Appli
 32 330 23.1 251 14 US-10-717-243-1 Sequence 259, App
 33 330 23.1 309 9 US-09-765-527-253 Sequence 253, App
 34 330 23.1 332 9 US-09-765-527-251 Sequence 251, App
 35 326 22.8 252 9 US-09-347-064-2 Sequence 2, Appli
 36 326 22.8 252 9 US-09-347-064-8 Sequence 8, Appli
 37 323 22.6 251 14 US-10-127-890-99 Sequence 3, Appli
 38 323 22.6 251 14 US-10-127-890-101 Sequence 101, App
 39 323 22.6 251 14 US-10-127-890-107 Sequence 107, App
 40 323 22.6 251 17 US-10-717-243-99 Sequence 99, Appli
 41 323 22.6 251 17 US-10-117-243-101 Sequence 101, Appli
 42 323 22.6 251 17 US-10-17-243-107 Sequence 107, App
 43 322 22.5 251 14 US-10-127-890-110 Sequence 107, App
 44 322 22.5 251 14 US-10-127-890-111 Sequence 111, App
 45 322 22.5 251 17 US-10-717-243-110 Sequence 110, App

ALIGNMENTS

RESULT 1
 US-09-905-247-1
 ; Sequence 1, Application US/03905247
 ; Publication No. US200401978521
 ; GENERAL INFORMATION:
 ; APPLICANT: KE, YI-BIAO
 ; INVENTION: Mutant Trichosanthin
 ; TITLE OF INVENTION: Mutant Trichosanthin
 ; FILE REFERENCE: 033991000J615-US0
 ; CURRENT APPLICATION NUMBER: US/09/905,247
 ; CURRENT FILING DATE: 2001-07-13
 ; PRIORITY APPLICATION NUMBER: CN 0019553.0
 ; PRIORITY FILING DATE: 2000-08-02
 ; PRIORITY APPLICATION NUMBER: CN 0103102.6
 ; PRIORITY FILING DATE: 2001-01-18
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 1
 ; LENGTH: 289
 ; TTYPE: PRT
 ; ORGANISM: Trichosanthes Kirilowii M.
 ; us-09-905-247-1

Query Match 99.5% ; Score 1424; DB 11; Length 289;
 Best Local Similarity 99.7%; Pred. No. 1_2e-128;
 Matches 288; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 1 MIRFLVLSLILTLFLTTPAVEGDVSRLSGATSSSYGVFTNLKPLNPKRKYDPLL 60
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 11 812.5 56.8 263 14 US-10-127-890-7 Sequence 34, Appli
 10 812.5 56.8 263 14 US-10-127-890-7 Sequence 7, Appli
 12 813.5 56.8 263 17 US-10-717-243-7 Sequence 5, Appli
 14 50.6 248 14 US-10-717-243-5 Sequence 5, Appli
 17 50.6 248 17 US-10-717-243-5 Sequence 5, Appli

QY 121 DAMRKVTLVPSGNYERI-QTAAGKIRENIPPLGLPALSITLFFYNNSAASALMVIQ 180

Db 121 DAMRKVTLPPSGNYERLQTAGKIRENIPGLPALSATITLYNNANSASALMVIOS 180

Qy 181 TSEARYKPFIEQIGKRVDTPLSLAISLENSWALSQIQTASTNGQFESPVULIN 240

Db 181 TSEARYKPFIEQIGKRVDTPLSLAISLENSWALSQIQTASTNGQFESPVULIN 240

Qy 241 AQNQRTITNDAGVVTNSNIALLNRMAMADDVPPMTQSGCCSYAL 289

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RESULT 2

US-10-280-679B-4

; Sequence 4, Application US/10280679B

; Publication No. US20030150019A1

; GENERAL INFORMATION:

; APPLICANT: Large Scale Biology Corporation

; TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors

; FILE REFERENCE: LSCB-0109-US03

; CURRENT APPLICATION NUMBER: US/10/280,679B

; CURRENT FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: 09/557,941

; PRIOR FILING DATE: 2000-04-24

; PRIOR APPLICATION NUMBER: 08/484,341

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: 07/923,692

; PRIOR FILING DATE: 1992-07-31

; PRIOR APPLICATION NUMBER: 07/600,244

; PRIOR FILING DATE: 1990-10-22

; PRIOR APPLICATION NUMBER: 07/641,617

; PRIOR FILING DATE: 1991-01-16

; PRIOR APPLICATION NUMBER: 07/737,899

; PRIOR FILING DATE: 1992-07-31

; PRIOR APPLICATION NUMBER: 07/739,143

; PRIOR FILING DATE: 1991-08-01

; PRIOR APPLICATION NUMBER: 07/310,881

; PRIOR FILING DATE: 1989-02-17

; PRIOR APPLICATION NUMBER: 07/160,766

; PRIOR FILING DATE: 1991-07-26

; PRIOR APPLICATION NUMBER: 07/739,143

; PRIOR FILING DATE: 1988-02-26

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 4

; LENGTH: 289

; TYPE: PRT

; ORGANISM: Chinese cucumber

US-10-280-725B-4

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Best Local Similarity 99.0%; Pred. No. 2.8e-128; 1; Indels 0; Gaps 0;

Matches 286; Conservative 2; Mismatches 2;

Indels 0; Gaps 0;

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Db 1 MIRFLVSLILTLFLTPAVEGDVSPRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60

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Db 61 RSSLPGSQRYALIHLTNYADETISVALIDTVNVIYGRAGDTSYFVNNEASATEAKVVK 120

Qy 121 DAMRKVTLPPSGNYERLQTAGKIRENIPGLPALSATITLYNNANSASALMVIOS 180

Db 121 DAMRKVTLPPSGNYERLQTAGKIRENIPGLPALSATITLYNNANSASALMVIOS 180

Qy 181 TSEARYKPFIEQIGKRVDTPLSLAISLENSWALSQIQTASTNGQFESPVULIN 240

Db 181 TSEARYKPFIEQIGKRVDTPLSLAISLENSWALSQIQTASTNGQFESPVULIN 240

Qy 241 AQNQRTITNDAGVVTNSNIALLNRMAMADDVPPMTQSGCCSYAL 289

Db 241 AQNQRTITNDAGVVTNSNIALLNRMAMADDVPPMTQSGCCSYAL 289

RESULT 4

US-09-792-793A-39

; Sequence 39, Application US/09792793A

; Patent No. US2002168370A1

; GENERAL INFORMATION:

; APPLICANT: McDonald, John R.

APPLICANT: Coggins, Philip
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
 TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
 FILE REFERENCE: 25020-601D
 CURRENT APPLICATION NUMBER: US/09/792,793A
 CURRENT FILING DATE: 2001-02-22
 NUMBER OF SEQ ID NOS: 93
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 39
 LENGTH: 247
 TYPE: PRT
 ORGANISM: Trichosanthus kirilowii
 US-09-792,793A-39

Query Match Best Local Similarity 85.3%; Score 1221; DB 9; Length 247; Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 DVSFRLSGATSSYGVFISNLKALPNERKLYDPLRSLPSQRYALIHLNYADETI 60

QY 84 SVAIDVTVNYIMGRAGTSYFNEEASATTAACVYKEDAMKRTQPLPSGNYERLQTAGK 143
 Db 61 SVAIDVTVNYIMGRAGTSYFNEEASATTAACVYKEDAMKRTQPLPSGNYERLQTAGK 120

QY 144 IRENIPIGLPLALDSAITLFLYVYVANSASAALMVIQTSSEARYKFEQOIGKRDVKTFL 203
 Db 121 IRENIPIGLPLALDSAITLFLYVYVANSASAALMVIQTSSEARYKFEQOIGKRDVKTFL 180

QY 204 PSAIISIENSWSALSKQIQTASTNGQFESPVLINAQNQRTVITNDAGVTSNALL 263
 Db 181 PSAIISIENSWSALSKQIQTASTNGQFESPVLINAQNQRTVITNDAGVTSNALL 240

QY 264 LNRRNMA 270
 Db 241 LNRRNMA 247

RESULT 5 US-10-375-209A-39
 Sequence 39, Application US/10375209A
 Publication No. US20030215421A1
 GENERAL INFORMATION:
 APPLICANT: McDonald, John R.
 APPLICANT: Coggins, Philip
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
 TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
 FILE REFERENCE: 25020-601E
 CURRENT APPLICATION NUMBER: US/10/375,209A
 CURRENT FILING DATE: 2003-02-24
 NUMBER OF SEQ ID NOS: 93
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 39
 LENGTH: 247
 TYPE: PRT
 ORGANISM: Trichosanthus kirilowii
 US-10-375-209A-39

Query Match Best Local Similarity 85.3%; Score 1221; DB 15; Length 247; Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSYGVFISNLKALPNERKLYDPLRSLPSQRYALIHLNYADETI 83
 Db 1 DVSFRLSGATSSYGVFISNLKALPNERKLYDPLRSLPSQRYALIHLNYADETI 60

US-10-127-890-6

Sequence 6, Application US/10127890
 Publication No. US2003016619A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

Carroll, Stephen F.

Studnicki, Gary M.

Proteins

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70-P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 247 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-127-890-6

Query Match Best Local Similarity 84.5%; Score 1209; DB 14; Length 247; Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 SVAIDVTVNYIMGRAGTSYFNEEASATEAKVYKEDAMKRTQPLPSQRYALIHLNYADETI 120

QY 144 IRENIPIGLPLALDSAITLFLYVYVANSASAALMVIQTSSEARYKFIQOIGKRDVKTFL 203
 24 DVSFRLSGATSSYGVFISNLKALPNERKLYDPLRSLPSQRYALIHLNYADETI 83

RESULT 7 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 ; US-10-717-243-6
 ; Query Match ; Score 1209; DB 17; Length 247;
 ; Best Local Similarity 84.5%; Score 1209; DB 17; Length 247;
 ; Matches 245; Conservative 0; Pred. No. 4.9e-108;
 ; Mismatches 2; Indels 0; Gaps 0;
 ; Db 144 IRENIPGLPALSATTLFYNNANSASAASALMVLQIOTSEARRYKFEQQIGKRVDKTFL 203
 ; 121 IRENIPGLPALSATTLFYNNANSASAASALMVLQIOTSEARRYKFEQQIGKRVDKTFL 180
 ; QY 204 PSLATISLENSWALSRSKQIQTASTNGQFESPVVLINAQNQRTITNDAGVTSNIALL 263
 ; 181 PSLATISLENSWALSRSKQIQTASTNGQFESPVVLINAQNQRTITNDAGVTSNIALL 240
 ; QY 264 LNRNNMA 270
 ; Db 241 LNRNNMA 247

RESULT 7 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 ; US-10-717-243-6 Application US/101717243
 ; Publication NO. US20050054835A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; Carroll, Stephen F.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; NUMBER OF SEQUENCES: 169
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US10/1717,243
 ; FILING DATE: 18-Nov-2003
 ; CLASSIFICATION: 530
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US10/8139,765
 ; FILING DATE: 15-APR-1997
 ; APPLICATION NUMBER: US 08/425,336
 ; FILING DATE: 18-APR-1995
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; APPLICATION NUMBER: US 07/887,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-8889
 ; TELEFAX: 312/707-9155
 ; TELEX: 650 388-1248
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 247 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear

RESULT 8 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 ; US-09-792-793A-34
 ; Sequence 34, Application US/09792793A
 ; Patent No. US20020168370A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McDonald, John R.
 ; INVENTOR: Coggins, Philip
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
 ; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
 ; FILE REFERENCE: 25020-601D
 ; CURRENT APPLICATION NUMBER: US/09/792,793A
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 93
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 34
 ; LENGTH: 247
 ; TYPE: PRT
 ; ORGANISM: Bryonia dioica
 ; US-09-792-793A-34

Query Match 74.8%; Score 1071; DB 9; Length 247;
 Best Local Similarity 86.2%; Pred. No. 9.9e-95;
 Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSYGVFTSNRKALPNERKLYDPLRSSLPGSORYALHINTNAYDETI 83
 ; 1 DVSFRLSGATSSYGVFTSNRKALPNERKLYDPLRSSLPGSORYALHINTNAYDETI 60
 ; Db 84 SVAIDVNVYMGYRAGDTSFNEASA-TEAKYVFKDAMKVTLPYSGNVERLQTAGK 143
 ; 61 SVAIDVNVYMGYRAGDTSFNEASA-TEAKYVFKDAMKVTLPYSGNVERLQTAGK 120
 ; Db 144 IRENIPGLPALSATTLFYNNANSASAASALMVLQIOTSEARRYKFEQQIGKRVDKTFL 203
 ; 121 IRENIPGLPALSATTLFYNNANSASAASALMVLQIOTSEARRYKFEQQIGKRVDKTFL 180
 ; QY 204 PSLATISLENSWALSRSKQIQTASTNGQFESPVVLINAQNQRTITNDAGVTSNIALL 263
 ; 181 PSLATISLENSWALSRSKQIQTASTNGQFESPVVLINAQNQRTITNDAGVTSNIALL 240
 ; QY 264 LNRNNMA 270
 ; Db 241 LNRNNMA 247

RESULT 9
 US-10-375-209A-34
 ; Sequence 34, Application US/10375209A
 ; Publication No. US20030215421A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McDonald, John R.
 ; APPLICANT: Coggins, Philip
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
 ; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
 ; FILE REFERENCE: 25020-601B
 ; CURRENT FILING DATE: 2003-02-24
 ; NUMBER OF SEQ ID NOS: 93
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 34
 ; LENGTH: 247
 ; TYPE: PRT
 ; ORGANISM: Bryonia dioica
 ; US-10-375-209A-34

Query Match 74.8%; Score 1071; DB 15; length 247;
 Best Local Similarity 86.2%; Pred. No. 9.9e-95;
 Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

Qy 24 DVSPRLSGATSSYGVFISNLKALPDKLPIPLRSPLPGSQRVALIHLNYABTI 83
 Db 1 DVSPRLSGATTSIGVFKNLQRLAIPYKRVVNLPLRSISGSGRYTLHLNYADBTI 60

Qy 84 SVAIDVDTNYYIMGRAFTSYFNEASEATAAKVFKDAMRKTLIPSGNYERLQTAGK 143
 Db 61 SVAIDVDTNYYIMGRAFTSYFNEASEATAAKVFKDAMRKTLIPSGNYERLQTAGK 120

Qy 144 IRENIPGLPALSATITLYFVNANSASALMLVLIQSTSEBARYKFEQQIGRVDKTFL 203
 Db 121 IRENIPGLPALSATITLYFVNANSASALMLVLIQSTSEBARYKFEQQIGRVDKTFL 180

Qy 204 PSLATISLENSWALSKIQIQLASTNGQFESPVVLINQNRQITITNDAGVTSNALL 263
 Db 181 PSLATISLENSWALSKIQIQLASTNGQFESPVVLINQNRQITITNDAGVTSNALL 240

Qy 264 LNPNMMA 270
 Db 241 LNPNMIA 247

RESULT 10
 US-10-127-890-7
 ; Sequence 7, Application US/10127890
 ; Publication No. US20030166196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; CARROLL, Stephen F.
 ; STUDNIKA, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; NUMBER OF SEQUENCES: 173
 ; PROTEINS
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10-127,890
 ; FILING DATE: 23-Apr-2002
 ; CLASSIFICATION: <Unknown>

RESULT 11
 US-10-717-243-7
 ; Sequence 7, Application US/10717243
 ; Publication No. US2005005483A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; CARROLL, Stephen F.
 ; STUDNIKA, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; NUMBER OF SEQUENCES: 169
 ; PROTEINS
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1996
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1999
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNichols, Janet M.
 REGISTRATION NUMBER: 32, 918
 REFERENCE/DOCKET NUMBER: 200-70-P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 ; US-10-127-890-7

Query Match 56.8%; Score 813.5; DB 14; Length 263;
 Best Local Similarity 63.8%; Pred. No. 7.2e-70;
 Matches 166; Conservative 38; Mismatches 55; Indels 1; Gaps 1;

Qy 24 DVSPRLSGATSSYGVFISNLKALPDKLPIPLRSPLPGSQRVALIHLNYABTI 83
 Db 1 DVSPRLSGATPSKSYGMFIDKDLNAPRKEVNIPLPSVSGAGRVLMLHFLNYDGTI 60

Qy 84 SVAIDVDTNYYIMGRAFTSYFNEASEATAAKVFKDAMRKTLIPSGNYERLQTAGK 143
 Db 61 TVAIDVDTNYYIMGRAFTSYFNEASEATAAKVFKDAMRKTLIPSGNYERLQTAGK 120

Qy 144 IRENIPGLPALSATITLYFVNANSASALMLVLIQSTSEBARYKFEQQIGRVDKTFL 203
 Db 121 PREKIPIGLPAQLSALIQLASTNGQFESPVVLINQNRQITITNDAGVTSNALL 180

Qy 204 PSLATISLENSWALSKIQIQLASTNGQFESPVVLINQNRQITITNDAGVTSNALL 263
 Db 181 PSLATISLENSWALSKIQIQLAQGNNGIFRTPIVLVNDKGNRQVQITITNDAGVTSNALL 240

Qy 264 LNPNMAMDD-DVPMQSP 282
 Db 241 LNPNMIAEGDNGDVSTHGF 260

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US10/717,243

FILING DATE: 18-Nov-2003

CLASSIFICATION: 530

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/839,765

FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

SEQUENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-717-243-7

Query Match 56.8%; Score 813.5; DB 17; Length 263; Best Local Similarity 63.8%; Pred. No. 7.2e-70; Matches 166; Conservative 38; Mismatches 55; Indels 1; Gaps 1;

QY 24 DVSFRLSGATSSYGVFISNLKALPNERKVDIPLRSLPGSQRVALIHLTNYADETI 83

1 DVSFRLSGADPRSYGMPFKDLRNALPFRKEVNYNPLIPSPSGAGRYLMLHFLFNGDKTI 60

QY 84 SVAIDNTVNYMGRAGDTSFVNFNEASATEAKYVFKDAMRKVTLPYSGNVRLQTAGK 143

61 TVADVDTVNYMGLADTTSVFPNEPAELAQVFRDARKITLPYSGNVRLQTAGK 120

Db 144 IRENPIGLPGLDAISLTFLYYNANSASAALMVLGOSTSEARYKPTEQQTGKVKDTPFL 203

QY 121 PREKIPIGLPLDAISLTFLYDSTAAGGALVLIQTAEARPKVIEQQIWERAYDEV 180

QY 204 PSLATISLENSSALSQKIQIASTNNGQFESPVVLINAQNQRTITWDAGVTSNIAL 263

181 PSLATISLENSSGLSKQIQLAQGNGNIFRTPVILVLDNGRNQVITVNTSKVTSNIOI 240

QY 264 LNRNNAAMMD-DVPMQSF 282

Db 241 IANTRNTAEGDNDGVDSTTHGP 260

RESULT 12

US-10-127-890-5

; Sequence 5, Application US/0127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; Carroll, Stephen F.

; Studnica, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 12-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1994

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

SEQUENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 248 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-127-890-5

Query Match 50.6%; Score 724.5; DB 14; Length 248; Best Local Similarity 59.0%; Pred. No. 2.5e-61; Matches 147; Conservative 49; Mismatches 50; Indels 3; Gaps 3;

QY 24 DVSFRLSGSSSTSFSKIGBKLPLSNGTWNLTILLSSASGASRYTLMISNGDKAI 60

1 DVRFSLSGSSSTSFSKIGBKLPLSNGTWNLTILLSSASGASRYTLMISNGDKAI 60

QY 84 SVAIDNTVNYMGRAGDTSFVNFNEASATEAKYVFKDAMRKVTLPYSGNVRLQTAGK 143

61 TVADVDTVNYMGLADTTSVFPNEPAELAQVFRDARKITLPYSGNVRLQTAGK 120

Db 144 IRENPIGLPGLDAISLTFLYYNANSASAALMVLGOSTSEARYKPTEQQTGKVKDTPFL 203

QY 121 PREKIPIGLPLDAISLTFLYDSTAAGGALVLIQTAEARPKVIEQQIWERAYDEV 180

QY 204 PSLATISLENSSALSQKIQIASTNNGQFESPVVLINAQNQRTITWDAGVTSNIAL 263

181 PSLATISLENSSGLSKQIQLAQGNGNIFRTPVILVLDNGRNQVITVNTSKVTSNIOI 240

QY 264 LNRNNAAMMD-DVPMQSF 282

Db 241 IANTRNTAEGDNDGVDSTTHGP 260

; Sequence 5, Application US/0127890

; Publication No. US20030166196A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; Carroll, Stephen F.

; Studnica, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

RESULT 13
 US-10-717-243-5
 Sequence 5 Application US/10717243
 Publication No. US20050054835A1
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 Carroll, Stephen F.
 Studnica, Gary M.
 ADDRESS: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/717,243
 FILING DATE: 18-NOV-2003
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/839,765
 FILING DATE: 15-APR-1997
 APPLICATION NUMBER: US 08/425,336
 FILING DATE: 18-APR-1995
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 APPLICATION NUMBER: US 07/987,567
 FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 248 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 ; US-10-717-243-5

Query Match 50.6%; Score 724.5; DB 17; Length 248;
 Best Local Similarity 59.0%; Pred. No. 2.5e-61; Mismatches 147; Conservative 49.4%; Indels 3; Gaps 3;

Matches 147; Conservatism 49.4%; Mismatches 50; Indels 3; Gaps 3;

QY 24 DYSFRSLSGATSSYYGVFISNLKALPNERKLYDPIPLRSSRSRQVALIHLTNYADBTI 83
 Db 1 DYRFLSQQSSSSTSYSKFIGDLRKLPSNGTVNVLNILLSSASGASRTYLMTLSNDGKAI 60

QY 84 SVAIDVNTVNYIMYRAGTSYFNEASAATAAKYVKPQKMRKUTPLPYSGNVYRLQTAGK 143
 Db 61 TVAVDVSQLYIMGKVLNSTSYFFNESDALKASQVFKGS-TIVLPLPSGNVYRLQTAGK 119

QY 144 IRENPIGLPLAQLSAILTFLYVMAASALAMLIQSTSSEARRYKFEQQIGKRVDTFL 203
 Db 120 ITRKIPGFLPQLSALTTFLYVOSTAAAFALVFLQTAGAERFKYEGQIQRISNOV 179

RESULT 14
 US-10-127-890-4
 Sequence 4 Application US/10127890
 Publication No. US20030166196A1
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 Carroll, Stephen F.
 Studnica, Gary M.
 ADDRESS: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/127,890
 FILING DATE: 23-APR-2002
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1995
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 APPLICATION NUMBER: US 07/987,567
 FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 263 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 ; US-10-127-890-4

Query Match 49.5%; Score 709; DB 14; Length 263;
 Best Local Similarity 61.6%; Pred. No. 8.5e-60; Mismatches 149; Conservative 30; Indels 61; Gaps 2; Gaps 2;

Matches 149; Conservatism 30; Mismatches 61; Indels 2; Gaps 2;

QY 24 DYSFRSLSGATSSYYGVFISNLKALPNERKLYDPIPLRSSRSRQVALIHLTNYADBTI 83
 Db 1 DVNFDLSTATAKYTKFIEDRATPPSHKVYDIPILYLISTSDSRFLBLTSVAYETI 60

us-10-717-243-4

QY 84 SVAIDTVVYIMYRAGDTSYFFNEASATEAKVFKDAMRKVTLPSGNVYERLOTAGK 143
 |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 61 SVAIDTVVYIMYRAGDTSYFFNEASATEAKVFKDAMRKVTLPSGNVYERLOTAGK 118
 |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 QY 144 IRENIDGLPALSAITTLYFVNANSASALMVLQSTSEARRYKFEQIGKRVDTKFL 203
 |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 119 IRENIDGLPALSAITTLYFVNANSASALMVLQSTSEARRYKFEQIGKRVDTKFL 178
 |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 QY 204 PSLATISLENSWALSKQIOLASTNGQFSPSPVULINAQNRVITNDAGVTSNALL 263
 |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 179 PSLATISLENSWALSKQIOLASTNGQFSPSPVULINAQNRVITNDAGVTSNALL 238
 |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 QY 264 LN 265
 |||||:
 Db 239 LN 240
 |||||:

RESULT 15
 US-10-717-243-4
 ; Sequence 4, Application US/10717243
 ; Publication No. US20050054835A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; Carroll, Stephen F.
 ; Studnitsky, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; NUMBER OF SEQNCES: 169
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60661
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US10/717,243
 ; FILING DATE: 18-Nov-2003
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/839,765
 ; FILING DATE: 15-APR-1997
 ; APPLICATION NUMBER: US 08/425,336
 ; FILING DATE: 18-APR-1995
 ; APPLICATION NUMBER: US 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; APPLICATION NUMBER: US 07/988,430
 ; FILING DATE: 09-DEC-1992
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McNicholas, Janet M.
 ; REGISTRATION NUMBER: 32,918
 ; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/707-8899
 ; TELEX: 650 388-1248
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 263 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 49.5%; Score 709; DB 17; Length 263;
 Best Local Similarity 61.6%; Pred. No. 8.5e-60; Indels 2; Gaps 2;
 Matches 149; Conservative 30; Mismatches 61; Indels 2; Gaps 2;
 Matches 149; Conservative 30; Mismatches 61; Indels 2; Gaps 2;
 QY 24 DVSFRSGATSSYGVFISURKALPNERKLYDPLRSLLPSGRVYALHLNTYADETI 83
 |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 1 DVNFPLSTATAKYKTFIEDFRATLPPSHKVYDPLYSTISDRFLIDLTSYAETI 60
 |||||:|||:|||:|||:|||:|||:|||:|||:
 QY 84 SVAIDTVVYIMYRAGDTSYFFNEASATEAKVFKDAMRKVTLPSGNVYERLOTAGK 143
 |||||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 61 SVAIDTVVYIMYRAGDTSYFFNEASATEAKVFKDAMRKVTLPSGNVYERLOTAGK 118
 |||||:|||:|||:|||:|||:|||:|||:|||:
 QY 144 IRENIDGLPALSAITTLYFVNANSASALMVLQSTSEARRYKFEQIGKRVDTKFL 203
 |||||:|||:|||:|||:|||:|||:|||:|||:
 Db 119 IRENIDGLPALSAITTLYFVNANSASALMVLQSTSEARRYKFEQIGKRVDTKFL 178
 |||||:|||:|||:|||:|||:|||:
 QY 204 PSLATISLENSWALSKQIOLASTNGQFSPSPVULINAQNRVITNDAGVTSNALL 263
 |||||:|||:|||:|||:|||:|||:|||:
 Db 179 PSLATISLENSWALSKQIOLASTNGQFSPSPVULINAQNRVITNDAGVTSNALL 238
 |||||:|||:|||:|||:
 QY 264 LN 265
 |||||:
 Db 239 LN 240
 |||||:

Search completed: April 12, 2005, 15:31:52
 Job time : 96.4347 SECs

PA	(NIEH/	NIE H.	PD	14-FEB-2001.
XX			XX	
PI	Ke Y., Nie H;		PI	02-AUG-2000; 2000CN-00119553.
XX			XX	
DR	WPI; 2002-227165/28.		PR	02-AUG-2000; 2000CN-00119553.
XX	N-PSDB; AAB95171.		XX	
PT	Mutant trichosanthin protein of low antigenicity useful for treating tumor e.g. leukemia, comprises a sequence of native trichosanthin with modification of at least one amino acid residue in three specific regions.		PA	(SHAN-) SHANGHAI INST CYTOBIOLOGY CHINESE ACADEMY.
PT			XX	Ke Y., Nie H;
XX			XX	WPI; 2001-291745/31.
DR	N-PSDB; AAB41473.		DR	N-PSDB; AAB41473.
PS	Example 1; FIG 1; 42pp; English.		XX	Trichosanthin mutant and its preparing process.
XX			XX	
CC	The invention relates to a mutant trichosanthin (MTCs) protein of low antigenicity comprising a sequence of native TCS with the modification of at least one amino acid residue in three regions which is 177-180, 203-227 and 230-244 and substantially retaining the biological activities of the native TCS. The MTCs protein, its fragment or derivative is useful as an therapeutic agent; or for preparing a medicament for treating viral disease e.g. acquired immunodeficiency syndrome (AIDS), tumour e.g. leukemia, for inducing abortion and/or treating ectopic pregnancy. The present sequence represents the native TCS		CC	The present invention describes a trichosanthin mutant which is prepared through the mutational deformation of the trichosanthin gene and using an expression system. The trichosanthin gene is isolated from Trichosanthus kirilowii (Mongolian snake-gourd). The trichosanthin mutant has several advantages including high biactivity, high selectivity to target, and strong kill action to cancer cells, virus and HIV. It can also be used for metaphase induced labour. The present sequence represents the exemplification of the present invention
CC	Sequence 289 AA;		CC	sequence of wild type trichosanthin which is given in the exemplification of the present invention
XX			XX	
Query	Match	100.0%; Score 1431; DB 5; Length 289;	Query	Match
Best	Local Similarity	100.0%; Pred. No. 1.1e-127;	Best	Local Similarity
Matches	289;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	99.9%; Pred. No. 1.7e-127;
Db			Db	
Qy	1	MIRFLVSLILITLFLTPAVEGDVDSRFLSGATSSSSYGVFSNLKALPNERKLYDPLL 60	Qy	1
Db	1	MIRFLVSLILITLFLTPAVEGDVDSRFLSGATSSSSYGVFSNLKALPNERKLYDPLL 60	Db	1
Qy	61	RSSLPGSQRVALIHLTNYADETISVAIDVTVNYIMGAGRDTSYFENASATEAKVFK 120	Qy	61
Db	61	RSSLPGSQRVALIHLTNYADETISVAIDVTVNYIMGAGRDTSYFENASATEAKVFK 120	Db	61
Qy	121	DAMRKVTLPLPSGNYERIQLTAGKIRENIPLGIPALDSAITLYFYNANSASALMVLQS 180	Qy	121
Db	121	DAMRKVTLPLPSGNYERIQLTAGKIRENIPLGIPALDSAITLYFYNANSASALMVLQS 180	Db	121
Qy	181	TSEAAKTFIQQIGKRVDTKFLPSLAIISLENSWSALSQKIQIASTNGQFESPVULIN 240	Qy	181
Db	181	TSEAAKTFIQQIGKRVDTKFLPSLAIISLENSWSALSQKIQIASTNGQFESPVULIN 240	Db	181
Qy	241	AQNQRTITNDAGVTSNIALLNRNMAAMDDVPMTOSGCGSYAI 289	Qy	241
Db	241	AQNQRTITNDAGVTSNIALLNRNMAAMDDVPMTOSGCGSYAI 289	Db	241
RESULT	2		RESULT	3
XX	AAB95129;		XX	AAR07514
XX	ID AAB95129 standard; protein; 289 AA.		XX	ID AAR07514 standard; protein; 289 AA.
AC			AC	
XX			XX	
DT	23-AUG-2001 (first entry)		DT	06-FEB-1991 (first entry)
XX			XX	
DE	Trichosanthes kirilowii trichosanthin (TCS) protein sequence.		DE	Trichosanthin from Trichosanthes kirilowii.
XX			XX	
KW	Trichosanthes kirilowii; trichosanthin; TCS; mutagenesis; mutation; MTCs; mutant of trichosanthin; Mongolian snake-gourd; biactivity; selectivity; cancer; virus; HIV; metaphase induced labour.		KW	trichosanthin (TCS); Human Immunodeficiency Virus; inhibition.
XX			XX	
OS	Trichosanthes kirilowii.		OS	Trichosanthes kirilowii.
XX			XX	
Key	Location/Qualifiers		Key	Location/Qualifiers
FH	Misc-difference 230 /note= "encoded by GCA"		FT	Region 1.-21 /label= "Signal Peptide
FT			FT	
XX	CN1283630-A.		XX	/note= "hydrophobic"
XX			XX	

PN W09012097-A.
 XX
 PD 18-OCT-1990.
 XX
 PP 04-APR-1989; 89US-00333184.
 XX
 PR 04-APR-1989; 89US-00333184.
 XX
 PA (GENE-) GENELABS INC.
 XX
 PI Piatek M, Chow T, Fry K;
 XX
 DR WPI; 1990-334847/44.
 XX
 DR N-PSDB; AAQ06343.
 XX
 PT Recombinant tri:trichosanthin protein - with selective inhibitory effect on
 PT viral expression in HIV infected T-cells or monocyte-macrophage.
 PS Example: FIG 4; 102pp; English.
 XX
 CC Genomic DNA was isolated from *T. kirilowii* leaves from Korea and a library
 CC was constructed. Clone pQ21D was identified as likely to contain a TCS-
 CC encoding sequence in its 4kb insert. The deduced amino acid sequence is
 CC identical to that of TCS purified from Cantonese *T. kirilowii* roots,
 CC except for 2 conservative substitutions, i.e. Thr for Ser at position
 CC 211 and Met for Thr at position 224. The Canton protein lacks the last 19
 CC C-terminal amino acid residues. See also AAQ06344-Q06351
 XX
 SQ Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 2; Length 289;
 Best Local Similarity 99.0%; Pred. No. 1; 2e-126;
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Ov 1 MIRPLVISLILILFLFLTPAVEDVSFLSGATSSSSYGVFISNLKALPNRKLVDPLL 60
 Db 1 MIRPLVISLILILFLFLTPAVEDVSFLSGATSSSSYGVFISNLKALPNRKLVDPLL 60
 Ov 61 RSSLPGSORYALIHLTNYADETISVAIDVNTVYIMGRDTSYFFNEASATEAKYVFK 120
 Db 61 RSSLPGSORYALIHLTNYADETISVAIDVNTVYIMGRDTSYFFNEASATEAKYVFK 120
 Ov 121 DAMRKVILPYSGVYERLQATAGKIRENPLGQALPSAIIYNNASALMVIQS 180
 Db 121 DAMRKVILPYSGVYERLQATAGKIRENPLGQALPSAIIYNNASALMVIQS 180
 Ov 181 TSEARYKPEIQQIGKRVDTKFLPSLAIISLENSWMSALSKQOIASTNGQESPVVILN 240
 Db 181 TSEARYKPEIQQIGKRVDTKFLPSLAIISLENSWMSALSKQOIASTNGQESPVVILN 240
 Ov 241 AQMQRVITNDAGVTSNIALLNRNNAADDVPMQTSQCGGSTL 289
 Db 241 AQMQRVITNDAGVTSNIALLNRNNAADDVPMQTSQCGGSTL 289

RESULT 4

AR25572 standard; protein: 289 AA.

XX AR25572;

AC AR25572;

DT 25-MAR-2003 (revised)

DT 13-JAN-1993 (first entry)

XX Trichosanthin from *Trichosanthes kirilowii*.

XX TCS; alpha-trichosanthin; Radix trichosanthin; abortifacient;

KW ribosome inactivating protein; RIP; HIV-infected human T cells;

KW human immunodeficiency virus.

XX Trichosanthes kirilowii.

XX Key Location/Qualifiers

FT Misc-difference 57
 FT /note= "Leu in previously published sequence"
 FT Misc-difference 60
 FT /note= "Ile in previously published sequence"
 FT Misc-difference 72
 FT /note= "Ile in previously published sequence"
 FT Misc-difference 82. .84
 FT /note= "region not present in previously published sequence"
 FT Misc-difference 92. .93
 FT /note= "previously published sequence contained a 10
 FT amino acid insert (DAGIQRNAV) between Val and Tyr"
 FT Misc-difference 143
 FT /note= "Gly in previously published sequence"
 FT Misc-difference 144
 FT /note= "Leu in previously published sequence"
 FT Misc-difference 196
 FT /note= "Ser in previously published sequence"
 FT Misc-difference 214. .215
 FT /note= "previously published sequence contained a Leu
 FT inserted between Ser and Trp"
 FT Misc-difference 216
 FT /note= "Leu in previously published sequence"
 FT Misc-difference 231
 FT /note= "Thr in previously published sequence"
 FT Misc-difference 234
 FT /note= "Ser in directly sequenced TCS"
 FT Misc-difference 246. .266
 FT /note= "21 amino acids not present in previously
 FT published sequence"
 FT Misc-difference 247
 FT /note= "Thr in directly sequenced TCS"
 XX PN US5124640-A.
 XX PD 07-JUL-1992.
 XX PR 04-APR-1990; 90US-00504775.
 XX PR 04-APR-1989; 89US-00333184.
 XX PR 07-SEP-1989; 89US-00404326.
 XX PA (GENE-) GENELABS INC.
 XX PI Piatek M, Chow TP, Fry K;
 XX DR WPI; 1992-249485/30.
 XX DR N-PSDB; AAQ25492.

PT Nucleic acid encoding trichosanthin protein - which can be used to
 PT inactivate ribosome(s) to inhibit protein synthesis or to inhibit HIV
 PT expression.

XX PS Claim 1; Fig 4; 53pp; English.

XX Trichosanthin protein was isolated from *T. kirilowii* root tuber and
 CC sequenced. The amino acid sequence was used to design sets of degenerate
 CC primers (see AR26505-8) for PCR amplification of the TCS coding
 CC sequence. The amplified product was used as a probe to isolate TCS coding
 CC sequence from *T. kirilowii* genomic libraries. One clone (pQ21D) contained
 CC a 4kb insert. The amino acid sequence deduced from the pQ21D insert
 CC differed from the purified TCS sequence by conservative substitutions at
 CC two positions (see Features Table). The differences are postulated to
 CC indicate minor variations between strains; the purified TCS was obtained
 CC from the Canton region of China and the genomic DNA was obtained from
 CC *T. kirilowii* leaves from Korea. The amino acid sequence was also found to
 CC differ substantially from the previously published TCS sequence (Acta
 CC Chemica Sinica, 43:943, 1984 and Pure and Appl. Chem., 58(5):789, 1986).
 CC The differences are shown in the Features Table. The present sequence
 CC agrees closely with X-ray diffraction data on crystallized TCS. The 21-
 CC amino acid insert also provides greater sequence homology with a number
 CC of RPs such as ricin A chain and abrin A chain than the previously
 CC published sequence. (Updated on 25-MAR-2003 to correct PP field.)"

XX	CC	Updated on 25-MAR-2003 to correct PR field.)
SQ	Sequence 289 AA;	
PT	selective inhibition of viral expression in <i>E. coli</i> - for use in the	
PT	recombinant Trichosanthin protein prodn. in HIV infected cells.	
PS	Disclosure; Fig 4; 37pp; English.	
XX	The sequence is identical to that of plant-derived TCS except for two	
XX	Best Local Similarity 99.0%; Pred. No. 1.2e-126; Length 289;	
CC	Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	
CC	Met for a Thr substitution at position 211 and a	
CC	secreted protein that undergoes post-translational processing at both the	
CC	amino and carboxy ends. The TCS coding sequence was amplified using the	
CC	primers of AQ31828-30. The amplified prod. has the sequence of AQ31827,	
CC	which was used as a probe. One isolate, pQ21D, comprises the sequence of	
CC	AQ31826. The recombinant TCS sequence may be used in the recombinant	
CC	prod. of TCS. TCS can be used for the selective inhibition of viral	
CC	expression in HIV-infected human T-cells or macrophages. (Updated on 25-	
CC	MAR-2003 to correct PR field.)	
SQ	Sequence 289 AA;	
PT	Query Match 99.2%; Score 1420; DB 2; Length 289;	
PT	Best Local Similarity 99.0%; Pred. No. 1.2e-126; Length 289;	
PS	Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	
XX	DB 181 TSEARRYKPIEQOIGKRVDKTFLPSLATISLENSWALSQKQIQTASTNGQFETPPVILIN 240	
XX	QY 241 AQNQRTVITNDAGVTSNIALLNRRNMAAMDDVPMTOFGCCSYAL 289	
XX	DB 241 AQNQRTVITNDAGVTSNIALLNRRNMAAMDDVPMTOFGCCSYAL 120	
XX	QY 61 RSSLPGSQRYALIHLNTADETISVALIDVTVYIMGYRAGDTSYFFNEASATEAKYVFK 120	
XX	DB 61 RSSLPGSQRYALIHLNTADETISVALIDVTVYIMGYRAGDTSYFFNEASATEAKYVFK 180	
XX	DB 121 DAMRKVTLIPSYGNVYERLQTAAGKIRENIPGLPALSITTFYNNANSAASALMVLQS 180	
XX	QY 181 TSEARRYKPIEQOIGKRVDKTFLPSLATISLENSWALSQKQIQTASTNGQFETPPVILIN 240	
XX	DB 181 TSEARRYKPIEQOIGKRVDKTFLPSLATISLENSWALSQKQIQTASTNGQFETPPVILIN 240	
XX	QY 61 RSSLPGSQRYALIHLNTADETISVALIDVTVYIMGYRAGDTSYFFNEASATEAKYVFK 120	
XX	DB 61 RSSLPGSQRYALIHLNTADETISVALIDVTVYIMGYRAGDTSYFFNEASATEAKYVFK 120	
XX	QY 121 DAMRKVTLIPSYGNVYERLQTAAGKIRENIPGLPALSITTFYNNANSAASALMVLQS 180	
XX	DB 121 DAMRKVTLIPSYGNVYERLQTAAGKIRENIPGLPALSITTFYNNANSAASALMVLQS 180	
XX	QY 181 TSEARRYKPIEQOIGKRVDKTFLPSLATISLENSWALSQKQIQTASTNGQFETPPVILIN 240	
XX	DB 181 TSEARRYKPIEQOIGKRVDKTFLPSLATISLENSWALSQKQIQTASTNGQFETPPVILIN 240	
XX	QY 241 AQNQRTVITNDAGVTSNIALLNRRNMAAMDDVPMTOFGCCSYAL 289	
XX	DB 241 AQNQRTVITNDAGVTSNIALLNRRNMAAMDDVPMTOFGCCSYAL 289	
OS	Synthetic.	
XX		
FT	Key peptide	location/Qualifiers
FT	peptide	1. .23
FT	/label=	sg peptide
FT	/note=	"putative N-terminal extension of the mature TCS"
FT	Protein	24. .270= mat_protein
FT	Misc-difference 234	
FT	/note=	"plant-derived TCS has Ser at this position"
FT	Misc-difference 247	
FT	/note=	"plant-derived TCS has Thr at this position"
FT	Protein	270. .289
FT	/note=	"putative C-terminal extension of the mature TCS"
XX	US5166056-A.	
XX		
XX	PD 24-NOV-1992.	
XX	PD 09-DEC-1991;	91US-00804293.
XX	PR 04-APR-1989;	89US-00333184.
XX	PR 07-SEP-1989;	89US-00404326.
PA	(GENE-) GENE LABS INC.	
XX		
XX	PI Piatak M, Chow TP;	
XX	WPI; 1992-414954/50.	
XX		
XX	RESULT 6	
XX	AAR55129	
XX	ID AAR55129 standard; protein; 289 AA.	
XX	AC AAR55129;	
XX	DT 27-AUG-2003 (revised)	
XX	DT 25-MAR-2003 (revised)	
XX	DT 11-JAN-1995 (first entry)	
XX	DE Alpha-trichosanthin coding.	
XX	Virus: recombination; plant virus; alpha trichosanthin; phenotype; alpha amylase; alpha haemoglobin; bromo mosaic virus; gemini virus; rice necrosis virus; tobamovirus; gene expression; chinese cucumber.	
OS	Trichosanthes kirilowii.	
XX		
PF	US5316931-A.	
XX		
XX	PD 31-MAY-1994.	
XX	PF 31-JUL-1992;	92US-00923692.
XX		
PR	26-FEB-1988;	88US-00160766.
PR	26-FEB-1988;	88US-00160771.
PR	15-JUL-1988;	88US-00219279.
PR	17-FEB-1989;	89US-00310881.
PR	05-MAY-1989;	89US-00347637.

PR	08-JUN-1989;	89US5-00363138.	XX	
PR	22-OCT-1990;	90US5-00002447.	PN	
PR	16-JAN-1991;	91US5-00641617.	XX	
PR	26-JUL-1991;	91US5-00737899.	PD	
PR	01-AUG-1991;	91US5-00739143.	XX	
PA	(BIOS-)	BIOSOURCE GENETICS CORP.	PP	
XX			06-JUN-1996;	
PT	Garger SJ,	Turpen AM,	95WO-US009299.	
PT	Turpen TH;		XX	
XX			07-JUN-1995;	
PT			95US-00483502.	
PA	(BIOS-)	BIOSOURCE TECHNOLOGIES INC.	XX	
XX			PI	
DR	Danson J,	Dawson MO,	Danson J;	
DR	Garger SJ,	Grill LK;	DR	
XX			WPI: 1994-176269/21.	
PT	New recombinant plant viral nucleic acid - capable of systemic infection and stable expression of non-native nucleic acid in plant host.	PS	N-PSDB; AAQ65573.	
XX				
CC	The alpha-trichosanthin gene may be inserted into a recombinant plant virus which can then be used to infect plants for the production of non-native products (in this case alpha-trichosanthin). Other genes which may be inserted into the virus are those which control a phenotypic trait, such as male sterility, or sequences encoding anti-sense RNA which can be useful to prevent the expression of undesired phenotypic traits. The recombinant virus is derived from a plus sense, single stranded virus selected from tobamovirus, bromo mosaic virus, rice necrosis virus or a gemini virus. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 27-AUG-2003 to correct OS field.)	PS		
XX				
CC	Sequence 289 AA;	SQ		
Query	Match	99.2%; Score 1420; DB 2; Length 289;		
Best	Local Similarity	99.0%; Pred. No. 1.2e-126;		
Matches	286;	Conservative 2;	Mismatches	1;
			Indels	0;
			Gaps	0;
QY	1	MIRFLVSLILILFLTPAVEGDVSFRISGATSSGGVFFISNRKALPNERKLYDPLL	60	XX
Db	1	MIRFLVSLILILFLTPAVEGDVSFRISGATSSGGVFFISNRKALPNERKLYDPLL	60	XX
QY	61	RSSLPGSQRYALIHLTNYADETISVAIDTVNTVYNGYRAGDTSYFPNEASATEAKYVFK	120	XX
Db	61	RSSLPGSQRYALIHLTNYADETISVAIDTVNTVYNGYRAGDTSYFPNEASATEAKYVFK	120	XX
QY	121	DAMRKVTLPSYGNVERLQTAGKIRENTPLGIPALDAITLTYFYNANSASA8MVLQ	180	XX
Db	121	DAMRKVTLPSYGNVERLQTAGKIRENTPLGIPALDAITLTYFYNANSASA8MVLQ	180	XX
QY	181	TSEARRYKPIEQQIGRKVDTKFLPSLAIISLENSWSALSKQILASTNGQFETPVVLIN	240	XX
Db	181	TSEARRYKPIEQQIGRKVDTKFLPSLAIISLENSWSALSKQILASTNGQFETPVVLIN	240	XX
QY	241	AQORVITTNVDAGVTSNIALLNRNMAADDVPMQTSFGCGSYAI	289	XX
Db	241	AQORVITTNVDAGVTSNIALLNRNMAADDVPMQTSFGCGSYAI	289	XX
RESULT	7			
ID	AAW10468	AAW10468 standard; protein; 289 AA.		
XX				
AC	AAW10468;			
XX				
DT	17-OCT-2003	(revised)		
DT	26-APR-1997	(first entry)		
XX				
DE	Chinese cucumber alpha-trichosanthin.			
XX				
RE	Recombinant viral nucleic acid; RNA virus; vector; tobacco mosaic virus; TMV; Chinese cucumber; alpha-trichosanthin; ribosome inactivating protein; antiviral; viricide; transgenic plant.			
XX				
OS	Trichosanthes kirilowii; Maximowicz.			
RESULT	8			
ID	AAW11870	AAW11870 standard; protein; 289 AA.		
XX				
AC	AAW11870;			
XX				
DT	27-AUG-2003	(revised)		
DT	25-MAR-2003	(revised)		
DT	21-APR-1997	(first entry)		
XX				
DE	Chinese cucumber alpha-trichosanthin.			

kw	Recombinant virus; alpha-haemoglobin; human; chinese cucumber; alpha trichosanthin; rice; alpha amylase; beta-haemoglobin; subgenomic promoter; coat protein.	Db	181 TSEAAKFKFIRQQIGKGRVKFLPLSLAISLNSALSQIQIASTNNQFETPVULIN 240
kw		Qy	241 AQNQVITNTNDAGVUTNTIAILNRRNMAAMDDVPMTOFGCCSYAL 289
xx	Cucumis sp.	Db	241 AQNQVITNTNDAGVUTNTIAILNRRNMAAMDDVPMTOFGCCSYAL 289
pn	US5589367-A.		
xx		RESULT 9	
pd	31-DEC-1996.	AY0174	
xx		ID AAY0174 standard; protein; 289 AA.	
pf	19-JAN-1994;	AY0174;	
xx	94US-00184237.	XX	
pr	26-FEB-1988;	88US-00160766.	
pr	26-FEB-1988;	88US-00160771.	
pr	15-JUL-1988;	88US-00219279.	
pr	17-FEB-1989;	89US-00310881.	
pr	05-MAY-1989;	89US-00347637.	
pr	08-JUN-1989;	89US-00363138.	
pr	22-OCT-1990;	90US-00600244.	
pr	16-JAN-1991;	91US-00641617.	
pr	26-JUL-1991;	91US-00737899.	
pr	01-AUG-1991;	91US-00739143.	
pr	31-JUL-1992;	92US-00923692.	
pa	(BIOS-) BIOSOURCE TECHNOLOGIES INC.		
pi	Garger SJ, Turpen AM, Grill LK, Grantham GL, Donson J, Dawson WO; Turpen TH;	XX	
pi	WPI; 1997-076845/07.	XX	
dr	N-PSDB; AAT61376.	XX	
xx		PD 30-MAR-1999.	
xx		XX 07-JUN-1995;	95US-00480432.
pt	Recombinant viral DNA for altering plant phenotype or protein prodn - contains non-native sub-genomic promoter for expression of heterologous protein and native promoter for expression of coat protein.	XX	
pt	Example 4; Col 45-46; 42pp; English.	PR	
xx	The sequences given in AAW1868-71 represent proteins which were produced by the recombinant viruses of the invention. The viruses are recombinant plant viruses which comprise a native plant virus subgenomic promoter, at least one non-native plant virus subgenomic promoter, and a sequence encoding a plant virus coat protein. These heterologous sequences are preferably under the control of the native promoter sequence. By using a plant virus existing cells can be altered with a new coding sequences without involving germ cell. The recombinant viruses are stable and can cause systemic infection, with stable expression/transcription in plants that are hosts for the non-native part of the vector. The nucleotide sequences encoding these protein preferably integrated in plant viruses having either the O-coat protein or the U1-coat protein gene. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)	PR	
cc	Sequence 289 AA;	PS	
cc	Query Match Best Local Similarity 99.2%; Score 1420; DB 2; Length 289; Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	XX	
cc	1 MRPFLVSLILITLFLTPPAVGDVDSRILSGATSSSYQVFSNLKALPNRKLQDPLL 60	CC	The invention relates to a recombinant plant viral nucleic acid derived from a plus sense, single stranded RNA plant virus. The recombinant plant viral nucleic acid comprises: (a) a first plant viral subgenomic promoter that is native to the plus sense, single stranded RNA plant virus and operably joined to a first nucleic acid expression sequence; and (b) a second plant viral subgenomic promoter that is non-native and is operably joined to a second nucleic acid expression sequence; where, (i) (a) and (b) are incapable of recombination with one another, (ii) either the first or the second nucleic acid expression sequence is a plant viral coat protein coding sequence. The recombinant plant viral nucleic acid allows the transcription of products in a host, such as therapeutic and other useful polypeptides or proteins e.g. enzymes, complex biomolecules and ribozymes. It also gives the option of applying the coding sequence to the desired organism, tissue, organ or cell is stable for the foreign coding sequences and is capable of Systemic infection in the plant host. The transformation and regeneration of target organisms become unnecessary. (Updated on 20-MAR-2003 to correct PR field.)
cc	1 MRPFLVSLILITLFLTPPAVGDVDSRILSGATSSSYQVFSNLKALPNRKLQDPLL 60	CC	
cc	61 RSSLPGSQRVALIHLTNADETISVALIDVNTYIMGRAGDTSYFFNEASATEAKVFK 120	CC	
cc	61 RSSLPGSQRVALIHLTNADETISVALIDVNTYIMGRAGDTSYFFNEASATEAKVFK 120	CC	
cc	121 DAMRKVTLPLPSGNVYERLQTAGKIRENPLGLPALSITLFLPYNNSAASALMVIQS 180	CC	
cc	121 DAMRKVTLPLPSGNVYERLQTAGKIRENPLGLPALSITLFLPYNNSAASALMVIQS 180	CC	
cc	181 TSEAAKFKFIRQQIGKGRVKFLPLSLAISLNSALSQIQIASTNNQFETPVULIN 240	CC	

XX	Sequence 289 AA;	PT	host plant and stable production of heterologous DNA useful for producing therapeutic proteins for treating e.g. AIDS.
SQ		XX	therapeutic proteins for treating e.g. AIDS.
Query Match	99.2%; Score 1420; DB 2; Length 289;	XX	therapeutic proteins for treating e.g. AIDS.
Best Local Similarity	99.0%; Pred. No. 1; 2e-126;	PS	Example 4; Col 45-48; 45pp; English.
Matches	286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	XX	Example 4; Col 45-48; 45pp; English.
QY	1 MIRFLVSLILTLFLTPAVEGDVSFRSLSGATSSSYGVFISNLRKALPNERKLYDPLL 60	CC	The present sequence represents chinese cucumber alpha-trichosanthin. The nucleic acid sequence can be expressed in the plant viral constructs of the invention. The specification describes a recombinant plant viral nucleic acid derived from a positive (+)-sense RNA plant virus comprising a native (+)-sense RNA plant virus promoter that is linked to an expression sequence and a heterologous (+)-sense RNA plant virus promoter that is linked to an expression sequence. The promoters are incapable of recombination with each other, and one of the expression sequences encodes a plant viral coat protein while the other is optionally a heterologous coding sequence. The plant viral nucleic acid is capable of systemic infection in a host plant. The viral construct is useful for the introduction and expression of non-viral foreign genes in plants and the production of e.g. potential AIDS therapeutic drugs. (Updated on 27-AUG-2003 to correct OS field.)
Db	1 MIRFLVSLILTLFLTPAVEGDVSFRSLSGATSSSYGVFISNLRKALPNERKLYDPLL 60	CC	The present sequence represents chinese cucumber alpha-trichosanthin. The nucleic acid sequence can be expressed in the plant viral constructs of the invention. The specification describes a recombinant plant viral nucleic acid derived from a positive (+)-sense RNA plant virus comprising a native (+)-sense RNA plant virus promoter that is linked to an expression sequence and a heterologous (+)-sense RNA plant virus promoter that is linked to an expression sequence. The promoters are incapable of recombination with each other, and one of the expression sequences encodes a plant viral coat protein while the other is optionally a heterologous coding sequence. The plant viral nucleic acid is capable of systemic infection in a host plant. The viral construct is useful for the introduction and expression of non-viral foreign genes in plants and the production of e.g. potential AIDS therapeutic drugs. (Updated on 27-AUG-2003 to correct OS field.)
QY	121 DAMRKVTLPSYGNVERLQTAGKIRENPLGLPALSATITLYFVNANSAASALMVQ 180	CC	The present sequence represents chinese cucumber alpha-trichosanthin. The nucleic acid sequence can be expressed in the plant viral constructs of the invention. The specification describes a recombinant plant viral nucleic acid derived from a positive (+)-sense RNA plant virus comprising a native (+)-sense RNA plant virus promoter that is linked to an expression sequence and a heterologous (+)-sense RNA plant virus promoter that is linked to an expression sequence. The promoters are incapable of recombination with each other, and one of the expression sequences encodes a plant viral coat protein while the other is optionally a heterologous coding sequence. The plant viral nucleic acid is capable of systemic infection in a host plant. The viral construct is useful for the introduction and expression of non-viral foreign genes in plants and the production of e.g. potential AIDS therapeutic drugs. (Updated on 27-AUG-2003 to correct OS field.)
Db	121 DAMRKVTLPSYGNVERLQTAGKIRENPLGLPALSATITLYFVNANSAASALMVQ 180	CC	The present sequence represents chinese cucumber alpha-trichosanthin. The nucleic acid sequence can be expressed in the plant viral constructs of the invention. The specification describes a recombinant plant viral nucleic acid derived from a positive (+)-sense RNA plant virus comprising a native (+)-sense RNA plant virus promoter that is linked to an expression sequence and a heterologous (+)-sense RNA plant virus promoter that is linked to an expression sequence. The promoters are incapable of recombination with each other, and one of the expression sequences encodes a plant viral coat protein while the other is optionally a heterologous coding sequence. The plant viral nucleic acid is capable of systemic infection in a host plant. The viral construct is useful for the introduction and expression of non-viral foreign genes in plants and the production of e.g. potential AIDS therapeutic drugs. (Updated on 27-AUG-2003 to correct OS field.)
QY	181 TSEARYKPIEQQIGRKVDTPLSLAISLENSWSALSQKQIASTNGQESPVLIN 240	CC	The present sequence represents chinese cucumber alpha-trichosanthin. The nucleic acid sequence can be expressed in the plant viral constructs of the invention. The specification describes a recombinant plant viral nucleic acid derived from a positive (+)-sense RNA plant virus comprising a native (+)-sense RNA plant virus promoter that is linked to an expression sequence and a heterologous (+)-sense RNA plant virus promoter that is linked to an expression sequence. The promoters are incapable of recombination with each other, and one of the expression sequences encodes a plant viral coat protein while the other is optionally a heterologous coding sequence. The plant viral nucleic acid is capable of systemic infection in a host plant. The viral construct is useful for the introduction and expression of non-viral foreign genes in plants and the production of e.g. potential AIDS therapeutic drugs. (Updated on 27-AUG-2003 to correct OS field.)
Db	181 TSEARYKPIEQQIGRKVDTPLSLAISLENSWSALSQKQIASTNGQESPVLIN 240	CC	The present sequence represents chinese cucumber alpha-trichosanthin. The nucleic acid sequence can be expressed in the plant viral constructs of the invention. The specification describes a recombinant plant viral nucleic acid derived from a positive (+)-sense RNA plant virus comprising a native (+)-sense RNA plant virus promoter that is linked to an expression sequence and a heterologous (+)-sense RNA plant virus promoter that is linked to an expression sequence. The promoters are incapable of recombination with each other, and one of the expression sequences encodes a plant viral coat protein while the other is optionally a heterologous coding sequence. The plant viral nucleic acid is capable of systemic infection in a host plant. The viral construct is useful for the introduction and expression of non-viral foreign genes in plants and the production of e.g. potential AIDS therapeutic drugs. (Updated on 27-AUG-2003 to correct OS field.)
QY	241 AQNRVITINVDAGVVTNSNIALLNRNMAADDVWMTQSFCGSVAL 289	CC	The present sequence represents chinese cucumber alpha-trichosanthin. The nucleic acid sequence can be expressed in the plant viral constructs of the invention. The specification describes a recombinant plant viral nucleic acid derived from a positive (+)-sense RNA plant virus comprising a native (+)-sense RNA plant virus promoter that is linked to an expression sequence and a heterologous (+)-sense RNA plant virus promoter that is linked to an expression sequence. The promoters are incapable of recombination with each other, and one of the expression sequences encodes a plant viral coat protein while the other is optionally a heterologous coding sequence. The plant viral nucleic acid is capable of systemic infection in a host plant. The viral construct is useful for the introduction and expression of non-viral foreign genes in plants and the production of e.g. potential AIDS therapeutic drugs. (Updated on 27-AUG-2003 to correct OS field.)
Db	241 AQNRVITINVDAGVVTNSNIALLNRNMAADDVWMTQSFCGSVAL 289	CC	The present sequence represents chinese cucumber alpha-trichosanthin. The nucleic acid sequence can be expressed in the plant viral constructs of the invention. The specification describes a recombinant plant viral nucleic acid derived from a positive (+)-sense RNA plant virus comprising a native (+)-sense RNA plant virus promoter that is linked to an expression sequence and a heterologous (+)-sense RNA plant virus promoter that is linked to an expression sequence. The promoters are incapable of recombination with each other, and one of the expression sequences encodes a plant viral coat protein while the other is optionally a heterologous coding sequence. The plant viral nucleic acid is capable of systemic infection in a host plant. The viral construct is useful for the introduction and expression of non-viral foreign genes in plants and the production of e.g. potential AIDS therapeutic drugs. (Updated on 27-AUG-2003 to correct OS field.)
RESULT 10		XX	Sequence 289 AA;
ID	AAW84192 standard; protein; 289 AA.	XX	Sequence 289 AA;
XX	AAW84192;	XX	Sequence 289 AA;
AC		XX	Sequence 289 AA;
XX		XX	Sequence 289 AA;
DT	27-AUG-2003 (revised)	XX	Sequence 289 AA;
DT	01-APR-1999 (first entry)	XX	Sequence 289 AA;
DE	Chinese cucumber alpha-trichosanthin.	XX	Sequence 289 AA;
XX		XX	Sequence 289 AA;
KW	Chinese cucumber; alpha-trichosanthin; plant virus;	XX	Sequence 289 AA;
KW	plant virus promoter; systemic infection; foreign gene expression;	XX	Sequence 289 AA;
KW	AIDS therapeutic drug.	XX	Sequence 289 AA;
XX		XX	Sequence 289 AA;
OS	Memordica cochinchinensis.	XX	Sequence 289 AA;
XX		XX	Sequence 289 AA;
PN	US5866785-A.	XX	Sequence 289 AA;
XX		XX	Sequence 289 AA;
PD	02-FEB-1999.	XX	Sequence 289 AA;
XX		XX	Sequence 289 AA;
PF	07-JUN-1995; 95US-00482920.	XX	Sequence 289 AA;
XX		XX	Sequence 289 AA;
PR	26-FEB-1988; 88US-00160766.	XX	Sequence 289 AA;
PR	26-FEB-1988; 88US-00160771.	XX	Sequence 289 AA;
PR	15-JUN-1988; 88US-00219279.	XX	Sequence 289 AA;
PR	17-FEB-1989; 89US-00310881.	XX	Sequence 289 AA;
PR	05-MAY-1989; 89US-00347637.	XX	Sequence 289 AA;
PR	08-JUN-1989; 89US-00363138.	XX	Sequence 289 AA;
PR	22-OCT-1990; 90US-00600244.	XX	Sequence 289 AA;
PR	16-JAN-1991; 91US-00641617.	XX	Sequence 289 AA;
PR	01-AUG-1991; 91US-00739143.	XX	Sequence 289 AA;
PR	31-JUL-1992; 92US-00923692.	XX	Sequence 289 AA;
PR	19-JAN-1994; 94US-00184237.	XX	Sequence 289 AA;
XX		XX	Sequence 289 AA;
PA	(BIOS-) BIOSOURCE TECHNOLOGIES INC.	XX	Sequence 289 AA;
XX		XX	Sequence 289 AA;
PT	Garger SJ, Turpen AM, Grill LK, Granthan GL, Donson J, Dawson WO;	XX	Sequence 289 AA;
PT	Turpen TH;	XX	Sequence 289 AA;
DR	WPI; 1999-142035/12.	XX	Sequence 289 AA;
DR	N-PSDB; AAX03385.	XX	Sequence 289 AA;
PR	Recombinant plant viral vector - that is capable of systemic infection in	XX	Sequence 289 AA;
PR		XX	Sequence 289 AA;
PR	26-FEB-1988; 88US-00160771.	XX	Sequence 289 AA;

PR 15-JUL-1988; 88US-00219379.
 PR 17-FEB-1989; 89US-00310881.
 PR 05-MAY-1989; 89US-00347637.
 PR 08-JUN-1989; 89US-00363138.
 PR 22-OCT-1990; 90US-0060244.
 PR 16-JAN-1991; 91US-00641617.
 PR 26-JUL-1991; 91US-00737899.
 PR 01-AUG-1991; 91US-00739143.
 PR 31-JUL-1992; 92US-00923692.
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Garger SJ, Grill LK, Turpen TH, Granthan GL, Dawson WO;
 PI Turpen AM, Donson J;
 XX WPI; 2000-338510/29.
 DR N-PSDB; AIA12393.
 XX
 PT Recombinant non-retroviral nucleic acid for producing proteins such as interleukins, melanin and vaccines, comprises subgenomic promoters linked to sequences coding for viral coat protein and heterologous proteins.
 PS Example 4; Col 61-62; 51pp; English.
 XX
 CC This invention describes a novel recombinant viral nucleic acid (I) from a non-retroviral (+) sense, single stranded animal RNA virus comprising a nucleic acid sequence coding for a viral coat protein regulated by a native subgenomic promoter and other two heterologous nucleic acid sequences regulated by two other subgenomic promoters. (I) is useful for expressing foreign genes e.g. genes inducing male sterility in plants. (I) is also useful for producing proteins such as interleukins, EPO (erythropoietin), CSF (colony stimulating factor), Factor VIII, hGH (human growth hormone), melanin, insulin, vaccines etc., and enzymes that are useful for stereo specific catalysis of organic compounds. (I) is stable and transcribed systematically. The dual subgenomic promoter system reduces the frequency of recombination thus reducing regeneration of the wild type virus. This sequence represents a chinese cucumber alpha-trichosanthin protein which is described in the method of the invention.
 CC (Updated on 06-AUG-2003 to correct OS field.)
 CC trichosanthin protein which is described in the method of the invention.
 CC
 XX SQ Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 3; Length 289;
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MIRFLVLISLILFLFLTPAVGSDVSPRLSGATSSYGVFISNLRKALPNRKLVDPLL 60
 Db 1 MIRFLVLISLILFLFLTPAVGSDVSPRLSGATSSYGVFISNLRKALPNRKLVDPLL 60
 Qy 61 RSSLPGSORYALHLTNYADEITISVAIDVTVNVMGRAGTSYFFNEASATEAKVFK 120
 Db 61 RSSLPGSORYALHLTNYADEITISVAIDVTVNVMGRAGTSYFFNEASATEAKVFK 120
 Qy 121 DANKKVTPYSGNVERQTAGKIRENTPLGIPALDAITTYNNASASALMVIOS 180
 Db 121 DANKKVTPYSGNVERQTAGKIRENTPLGIPALDAITTYNNASASALMVIOS 180
 Qy 181 TSEARYKTFIEQDQIGKRDVKTEPLSLATISLENSWMSLSKQIASTNGQFESPVILN 240
 Db 181 TSEARYKTFIEQDQIGKRDVKTEPLSLATISLENSWMSLSKQIASTNGQFESPVILN 240
 Qy 241 AQNQRVITNDAGVTSNIAUILLNRMAMDDDVMTQSGCGSYAL 289
 Db 241 AQNQRVITNDAGVTSNIAUILLNRMAMDDDVMTQSGCGSYAL 289
 XX
 RESULT 12
 ADH44106 standard; protein; 289 AA.
 ID ADH44106
 XX
 AC ADH44106;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Chinese cucumber alpha-trichosanthin.
 XX
 RVNA; cis-acting replication; RNA plant virus; capped RNA molecule;
 KW coat gene; movement protein gene; subgenomic promoter;
 KW herbicide resistance; extreme temperature resistance; drought;
 KW osmotic stress; pests resistance; male sterility; female sterility;
 KW yield; collagenase cleavage site; Chinese cucumber; alpha-trichosanthin;
 KW enzyme; plant.
 XX OS Trichosanthes kirilowii.
 XX
 PR Key Location/Qualifiers
 PR Peptide 1..23
 PR PT /note= "Signal peptide"
 PR PT Protein 24..289
 PR /note= "Mature alpha trichosanthin"
 XX US2003150019-A1.
 PR DD 07-APR-2003.
 XX PR 24-OCT-2002; 2002US-00280679.
 XX PR 26-FEB-1988; 88US-00160766.
 PR 26-FEB-1988; 88US-00160771.
 PR 15-JUL-1988; 88US-00219279.
 PR 22-OCT-1990; 90US-00600244.
 PR 16-JAN-1991; 91US-00641617.
 PR 26-JUL-1991; 91US-00737899.
 PR 01-AUG-1991; 91US-00739143.
 PR 31-JUL-1992; 92US-00923692.
 PR 07-JUN-1995; 95US-00434341.
 PR 24-APR-2000; 2000US-00577941.
 XX PR (LARG-) LARGE SCALE BIOLOGY CORP.
 XX PR Turpen TH, Turpen AM, Garger SJ, Grill LK, Donson J, Dawson WO;
 PR Granthan GL;
 XX DR N-PSDB; ADH44105.
 XX PR New recombinant viral RNA molecules, useful in modifying a plant host cell, genetically or phenotypically, e.g. male sterility or improved resistance to pests or diseases, or for producing pharmaceuticals, PT hormones or antibodies.
 XX
 PR Example 4; SEQ ID NO 4; 50pp; English.
 XX
 CC The invention relates to an RNA molecule (RVNA) comprising a cis-acting replication element from a positive strand RNA plant virus capable of replication in a plant cell and comprising an exogenous RNA segment capable of expressing its function in a host cell. The exogenous RNA segment is located in a region of the RNA molecule able to tolerate the segment without disrupting RNA replication in the absence of a trans-acting replication element in the host cell. Also included are a capped RNA molecule capable of infecting a host plant cell (where the capped RNA molecule: (a) comprises a cis-acting replication element derived from a positive strand RNA plant virus, has no extraneous non-viral sequences between the cap site and the 5' terminus of the viral sequence, and further comprises an exogenous RNA segment capable of expressing its function in a host cell in a region of the capped RNA molecule able to tolerate the segment without disrupting RNA replication of the capped RNA molecule in the absence of a trans-acting replication element in the host cell; or (b) has no extraneous non-viral sequences between the cap site and the 5' terminus of the viral sequence, and where the capped RNA molecule comprises the entire genome of the positive strand RNA virus, such as luteovirus, potexvirus, potyvirus, tombusvirus, tymovirus and tobamovirus, camovirus, or sobemovirus, and an exogenous RNA segment capable of expressing its function in a host cell, where the exogenous RNA segment inserted into the genome of the positive strand RNA virus at

a gene site consisting of a coat gene site, a movement protein gene site, or another gene site under the control of a subgenomic promoter, which is one of at least two subgenomic promoters present in the virus), a DNA transcription vector comprising cDNA having one strand complementary to the (capped) RNA molecule cited above and methods of modifying a host cell, genetically or phenotypically (comprising introducing into the cell the (capped) RNA molecule cited above, where the exogenous RNA segment confers a detectable trait in the host cell which modifies the host cell). The cis-acting replication element is derived from a monopartite plant virus, tobamovirus, or tobacco mosaic virus. The (capped) RNA molecules and DNA transcription vectors are useful in modifying a host cell, genetically or phenotypically, e.g., improved tolerance to herbicides, extremes of heat or cold, drought or osmotic stress, improved resistance to pests or diseases, male or female sterility, or improved yield. The RNA molecules are also useful for transcription or expression of foreign genes in the host to produce the desired product, such as pharmaceuticals, hormones, antibiotics, pigments, or antibodies. The present sequence is encoded by the Chinese cucumber, alpha-trichosanthin cDNA, which was used as the exogenous RNA in an RNA of the invention.

Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 7; Length 289;
Best Local Similarity 99.0%; Pred. No. 1.2e-126; Mismatches 1; Indels 0; Gaps 0; Matches 286; Conservative 2; MisMatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVLSLILTLFLTPAVEGDVSFRISGATSSSYGVFISNRKALPNERKLYDPLL 60
Db 1 MIRFLVLSLILTLFLTPAVEGDVSFRISGATSSSYGVFISNRKALPNERKLYDPLL 60
QY 61 RSSLPGSQRYALHLTYNADETISVALIDTVNYIMGRRAGDTSYFFNEASATEAKYVFK 120
Db 61 RSSLPGSQRYALHLTYNADETISVALIDTVNYIMGRRAGDTSYFFNEASATEAKYVFK 120
QY 121 DAMRKVTLPSGNTVERQIAGKIRENTPLGIPALDAITLTYNANSASALMVIJOS 180
Db 121 DAMRKVTLPSGNTVERQIAGKIRENTPLGIPALDAITLTYNANSASALMVIQOS 180
QY 181 TSEARKKIEQOIGKRVDTKFLPSLAIISLENSWALSKQIQTASTNGQFSPVVLIN 240
Db 181 TSEARKKIEQOIGKRVDTKFLPSLAIISLENSWALSKQIQTASTNGQFSPVVLIN 240
QY 241 AQNRQVITINVDAGVTSNITALLNRRNAMDDDPVMTQSGFGGSYAI 289
Db 241 AQNRQVITINVDAGVTSNITALLNRRNAMDDDPVMTQSGFGGSYAI 289

RESULT 13

ADO43821; ID ADO43821 standard; protein; 289 AA.
XX AC ADO43821;
XX DT 15-JUL-2004 (first entry)
XX DE Chinese cucumber alpha-trichosanthin.

XX KW recombinant viral nucleic acid; animal virus; subgenomic promoter; viral coat protein; IL-1; IL-2; IL-3; IL-4; IL-5; IL-6; IL-7; IL-8; IL-9; IL-10; IL-11; IL-12; EPO; G-CSF; GM-CSF; M-CSF; Factor VIII; Factor IX; tissue plasminogen activator; human growth hormone; neuro-Polypeptide; melanin; lipase; hormone; pharmaceutical; antibiotic; vaccine; insulin; chinese cucumber; alpha-trichosanthin.
OS Trichosanthes kirilowii.
XX PN US2004049025-A1.
XX PD 11-MAR-2004.
XX PF 24-OCT-2002; 2002US-00280725.
XX

PR 26-FEB-1988; 88US-00160766.
PR 26-FEB-1988; 88US-00160771.
PR 15-JUL-1988; 89US-00219279.
PR 17-FEB-1989; 89US-00310881.
PR 05-MAY-1989; 89US-00347637.
PR 08-JUN-1989; 89US-00363138.
PR 22-OCT-1990; 90US-00600244.
PR 16-JAN-1991; 91US-00641617.
PR 26-JUL-1991; 91US-0073899.
PR 01-AUG-1991; 91US-00739143.
PR 31-JUL-1992; 92US-00923692.
PR 07-JUN-1995; 95US-00484341.
PR 24-APR-2000; 2000US-00557941.
PA (LARG-) LARGE SCALE BIOLOGY CORP.
PI Donson J, Dawson WO, Grantham GL, Turpen TH, Turpen AM;
PI Garger SJ, Grill LK;
DR WPI; 2004-238515/22.
DR N-PSDB; ADO43820.
XX PT New recombinant viral nucleic acid derived from an animal virus having a native subgenomic promoter, useful in production of products such as interleukins, enzymes, and hormones.
PS XX Example 4; SEQ ID NO 4; 49P; English.

QY The invention describes a recombinant viral nucleic acid derived from an animal virus possessing a native subgenomic promoter. The recombinant viral nucleic acid sequence that codes for a viral coat protein whose nucleic acid sequence that codes for a viral coat protein whose transcription is regulated by the first viral subgenomic promoter; a second viral sub genomic promoter; and a second nucleic acid sequence whose transcription is regulated by the second viral sub genomic promoter, where the first and second viral subgenomic promoters possess different nucleic acid sequences relative to each other, and the second nucleic acid sequence is upstream to the first nucleic acid sequence. Also described is a non-human host animal infected by a viral vector comprising the recombinant viral nucleic acid; and a process for transcribing a nucleic acid sequence in a non-human host animal. The recombinant viral nucleic acid is useful in sustained systemic transcription of nucleotide sequences within host cells and in producing gene products, e.g. IL-1-12, EPO, G-CSF, GM-CSF, M-CSF, Factor VIII, Factor IX, tissue plasminogen activator, human growth hormone, receptors, receptor antagonists, antibodies, neuro-polypeptides, melanin, lipase, hormones, pharmaceuticals, antibiotics, vaccines and insulin within a host animal. This is the amino acid sequence of Chinese cucumber alpha-trichosanthin that can be incorporated into the recombinant viral protein of the invention.

XX Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 8; Length 289;
Best Local Similarity 99.0%; Pred. No. 1.2e-126; Mismatches 1; Indels 0; Gaps 0; Matches 286; Conservative 2; MisMatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVLSLILTLFLTPAVEGDVSFRISGATSSSYGVFISNRKALPNERKLYDPLL 60
Db 1 MIRFLVLSLILTLFLTPAVEGDVSFRISGATSSSYGVFISNRKALPNERKLYDPLL 60
QY 61 RSSLPGSQRYALHLTYNADETISVALIDTVNYIMGRRAGDTSYFFNEASATEAKYVFK 120
Db 61 RSSLPGSQRYALHLTYNADETISVALIDTVNYIMGRRAGDTSYFFNEASATEAKYVFK 120
QY 121 DAMRKVTLPSGNTVERQIAGKIRENTPLGIPALDAITLTYNANSASALMVIJOS 180
Db 121 DAMRKVTLPSGNTVERQIAGKIRENTPLGIPALDAITLTYNANSASALMVIQOS 180
QY 181 TSEARKKIEQOIGKRVDTKFLPSLAIISLENSWALSKQIQTASTNGQFSPVVLIN 240
Db 181 TSEARKKIEQOIGKRVDTKFLPSLAIISLENSWALSKQIQTASTNGQFSPVVLIN 240

Qy	241	AQNQVITNDAGVTSNIALLNRMNAMDDVPMTOQFCGGSYAL	289	Qy	121	DAMRKVTLPLYSQNYERLQTAAGKIRENIPGLPGLDASITLFFYNNASASALMILQS	180
Db	241	AQNQVITNDAGVTSNIALLNRMNAMDDVPMTOQFCGGSYAI	289	Db	121	DAMRKVTLPLYSQNYERLQTAAGKIRENIPGLPGLDASITLFFYNNASASALMILQS	180
RESULT 14				Qy	181	TSEAAKTFIPOQIGRVDKTFPLPSAATIENSNSALSKQIOIATNNQFESPVTLIN	240
ID	AAR32986	standard; protein; 289 AA.		Db	181	TSEAAKTFIPOQIGRVDKTFPLPSAATIENSNSALSKQIOIATNNQFESPVTLIN	240
XX	AAR32986;			Qy	241	AQNQVITNDAGVTSNIALLNRMNAMDDVPMTOQFCGGSYAL	289
AC				Db	241	AQNQVITNDAGVTSNIALLNRMNAMDDVPMTOQFCGGSYAI	289
XX				DE			
DT	27-AUG-2003	(revised)		DT	25-MAR-2003	(revised)	
		17-JUN-1993	(first entry)				
XX				DE	Encodes chinese cucumber alpha-tricosanthin.		
KW	Recombinant products; commercial production; fermentation; biosynthesis; natural products; recombinant proteins; product expression; protein expression; expressed proteins.			KW			
XX				DE			
KW	Cucurbitaceae.			DN			
OS				PN			
XX	W09303161-A1.			XX			
PD	18-FEB-1993.			PD	18-FEB-1993.		
XX				XX			
PF	31-JUL-1992;	92WO-US006359.		XX			
XX	01-AUG-1991;	91US-00739143.		XX			
PR				XX			
XX	(DONS/)	DONSON J.		XX			
PA	(DAWS/)	DANSON W O.		XX			
PA	(GRAN/)	GRANTHAM G L.		XX			
PA	(TURP/)	TURPEN T H.		XX			
PA	(TURP/)	TURPEN A M.		XX			
PA	(GARG/)	GARGER S J.		XX			
PA	(GRIL/)	GRILLE L K.		XX			
XX				XX			
PI	Donson J,	Dawson WO,	Grantham GL,	XX			
PI				XX			
XX	PI	Garger SJ,	Grille LK;	XX			
XX	PT			XX			
DR	WPI;	1993-07651809.		XX			
XX	N-PSDB;	AAQ37679.		XX			
PS	Example 4; Page 96;	30pp;	English.	XX			
XX				XX			
CC	This sequence represents chinese cucumber alpha-tricosanthin. The coding sequence is inserted into a recombinant plant viral nucleic acid which is then used to express a recombinant product (in this case alpha-tricosanthin) in a plant. The plant viral sequence may be from tobacco mosaic, cucumber green mottle, cowpea mosaic, brom mosaic, broad bean mottle, rice necrosis, geminiviruses, tomato golden mosaic, Cassava latent and maize streak viruses. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 25-MAR-2003 to correct OS field.)			XX			
SQ	Sequence 289 AA;			XX			
Query Match	99.0%	Score 1417;	DB 2;	Length 289;	XX		
Best Local Similarity	98.6%	Pred. No. 2.3e-126;			XX		
Matches	285;	Conservative	3;	Mismatches 1;	Indels 0;	Gaps 0;	
Qy	1	MIRFLVLSLILTLFLTFPAVEGDVPSFLSGATSSSSYGVFTSNLRKALPNERKLYDIPLL	60	Qy	1	MIRFLVLSLILTLFLTFPAVEGDVPSFLSGATSSSSYGVFTSNLRKALPNERKLYDIPLL	60
Db	1	MIRFLVLSLILTLFLTFPAVEGDVPSFLSGATSSSSYGVFTSNLRKALPNERKLYDIPLL	60	Db	1	MIRFLVLSLILTLFLTFPAVEGDVPSFLSGATSSSSYGVFTSNLRKALPNERKLYDIPLL	60
Qy	61	RSSLPGSQRYALIHLTNYADETISVA,DVTNYIMGRAFTSYFNEASATEAKYVK	120	Qy	61	RSSLPGSQRYALIHLTNYADETISVA,DVTNYIMGRAFTSYFNEASATEAKYVK	120
Db	61	RSSLPGSQRYALIHLTNYADETISVA,DVTNYIMGRAFTSYFNEASATEAKYVK	120	Db	61	RSTLQSGQRYALIHLTNYADETISVA,DVTNYIMGRAFTSYFNEASATEAKYVK	120

QY 121 DAMKVTLPSGNVERLQTAGKIRENPLGLPAUDSAITLTYNANSASALMVLIQS 180
Db 121 DAQKVTLPSGNVERLQAGKIRENPLGLPAUDSAITLTYNANSASALMVLIQS 180
QY 181 TSEARYKEIEQQTGKRVDTKFLPSLAIISLENSWSALSKQIASTNGQFSPVULIN 240
Db 181 MSEARRYKEIEQQIGRRDKFLPSLAIISLENSWSALSKQIASTNGQFSPVULIN 240
QY 241 ACONRVTITNDAGVTSNIALLNRNMAAMDDVPMQSRCGGSYAI 289
Db 241 ACGORVTITNDAGVTSNIALLNRNMAVIDDHVPMQSRCGGSYAI 289

Search completed: April 12, 2005, 15:09:59
Job time : 133.481 secs

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OM protein - protein search, using SW model

Run on: April 12, 2005, 14:56:17 ; Search time 125.09 Seconds
(without alignments)
1183.080 Million cell updates/sec

Title: US-09-905-247a-1
perfect score: 1431
Sequence: 1 MIRFLVLSMLTFLTPA.....AAMDDDVPMTQSFGCGSYAL 289

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : UniProt 03:
1: uniprot_sprot:
2: uniprot_trembl:
SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

32	414	28.9	580	2	Q94BW4	Q94bw4 cinnamomum
33	410	28.7	580	2	Q94BW3	Q94bw3 cinnamomum
34	407.5	28.5	575	2	Q84J1J	Q84J1J gynostemma
35	407	28.4	581	2	Q94BW5	Q94bw5 cinnamomum
36	403.5	28.2	277	2	Q8GW09	Q8gw09 gynostemma
37	403.5	28.2	549	2	Q8FV22	Q8fv22 cinnamomum
38	401.5	28.1	277	2	Q8AJR1	Q84Jrl gynostemma
39	400.5	28.0	277	2	Q8GW11	Q8gw11 gynostemma
40	395.5	27.7	564	1	P06750	P06750 ricinus com
41	395.5	27.6	277	2	Q8H1Y5	Q8h1y5 gynostemma
42	393.5	27.5	136	2	Q8AIJ0	Q841j0 cucurbita m
43	388.5	27.4	136	2	Q8AV19	Q841j9 cucurbita m
44	388.5	27.1	2	Q8EV10	Q8gv10 gynostemma	
45	384.5	26.9	136	2	Q8S2R5	Q8s2r5 cucurbita m

RESULT 1

ID	NAME	STANDARD	PRT;	289 AA.
P09989	RIFTTRIKI			
DT	01-MAR-1989	(Rel. 10, Created)		
DT	01-NOV-1990	(Rel. 16, Last sequence update)		
DT	25-OCT-2004	(Rel. 45, Last annotation update)		
DE	Ribosome-inactivating protein alpha-trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase) (Alpha-TCSI).			
OS	Trichosanthes kirilowii (Mongolian snake-gourd); Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;			
OC	euroids; I; Cucurbitales; Cucurbitaceae; Trichosanthes.			
OX	NOBI_TaxID=3677;			
RN				
RP				
RC	STRAIN=Maximowicz; PubMed=1999291; DOI=10.1016/0378-1119(91)90061-F;			
RA	Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.; "Cloning of trichosanthin cDNA and its expression in Escherichia			
RT	coli";			
RT	[1]			
RN	SEQUENCE FROM N.A.			
RP	MDLINE=91153657; PubMed=91153657;			
RC	MDLINE=90256789; PubMed=90256789;			
RA	Collins E.J., Robertus J.D., Iopresti M., Stone K.L., Williams K.R., Wu P., Hwang K., Piatak M.;			
RT	"Primary amino acid sequence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin.";			
RT	J. Biol. Chem. 265:8665-8669 (1990).			
RT	[4]			
RN	SEQUENCE OF 24-270.			
RP	MDLINE=90256789; PubMed=90256789;			
RC	MDLINE=90256789; PubMed=90256789;			
RA	Tian G.Y., Ni C.Z., "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application.";			
RT	J. Biol. Chem. 265:8665-8669 (1990).			
RT	[5]			
RN	STRUCTURE OF 24-270.			
RP	MDLINE=90256789; PubMed=90256789;			
RA	Wang Y., Qian R.Q., Gu Z.W., Zhang L.Q., Xia Z.X., Tian G.Y., Ni C.Z., "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application.";			
RT	J. Biol. Chem. 265:8665-8669 (1990).			
RT	[6]			

Result No.	Score	Query	Match Length	DB ID	Description
1	1429	99.9	289	1 RIFTTRIKI	P09989 trichosanthin
2	1426	99.7	289	2 Q84S98	Q94AV8 trichosanthin
3	1425	99.6	289	2 Q94KE8	Q94KE6 trichosanthin
4	1415	98.9	289	2 Q412I6	Q412I6 trichosanthin
5	1384	96.7	289	1 RIPS TRIKI	P24478 trichosanthin
6	1269	88.7	270	1 Q416J1	Q416J1 trichosanthin
7	1264	88.3	270	2 Q6PQ7	Q8PQ95 trichosanthin
8	1260	88.1	270	2 Q8LPV7	Q8LPV7 trichosanthin
9	1195	83.5	247	2 Q6BBQ4	Q6bbq4 trichosanthin
10	1187	82.9	247	2 Q9LRE3	Q9lre3 trichosanthin
11	1171.5	81.9	290	1 RIPI_BRYDI	P3185 bryonia dio
12	866.5	80.6	286	1 RIPI_MOMCH	P16094 momordica c
13	809.5	56.6	277	1 RIPI_LUFCY	Q00465 luffa cylin
14	782	54.6	278	2 Q00S80	Q00980 luffa cylin
15	764	53.4	286	1 RIPI_MOMCH	P24817 momordica c
16	762	53.2	286	1 RIPI_MOMBA	P23339 momordica b
17	743	51.9	285	1 RIPI_CUCF1	Q9trx4 cucurbita b
18	711	49.7	264	1 Q68J5	Q68J5 cucurbita b
19	682.5	47.7	294	1 RIPI_TRIAN	Q664J5 momordica c
20	680	47.5	250	1 RIPI_LUFCY	P22851 trichosanthin
21	540.5	37.8	282	1 RIPI_BRYDI	P98184 bryonia dio
22	476.5	33.3	136	2 Q8SAD7	Q8gt32 sambucus ni
23	439.5	30.7	563	2 Q8GT32	Q8gt32 sambucus ni
24	435.5	30.4	563	2 Q94S92	Q94S92 sambucus ni
25	434.5	30.4	563	1 NIGB_SAMNT	P3183 sambucus ni
26	432.5	30.2	563	2 Q04367	Q04367 sambucus ni
27	425	29.7	541	2 Q41174	Q41174 ricinus com
28	421	29.4	576	1 RIC1_RICCO	P02879 ricinus com
29	418.5	29.2	275	2 Q8HY4	Q8H1Y4 gynostemma
30	416.5	29.1	564	2 Q9AVR2	Q9avr2 sambucus eb
31	415.5	29.0	136	2 Q8SAGO	Q8sago benincasa h

RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=9534383; Published=7/19/07;
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
 RT "Studies on crystal structures, active-centre geometry and
 depurinating mechanism of two ribosome-inactivating proteins.";
 RL Biochem. J. 309:285-288 (1995).
 CC -!- FUNCTION: Trichosanthin is an abortion-inducing protein. It is
 capable of inhibiting HIV-1 infection and replication. It
 inactivates eukaryotic 60S ribosomal subunits.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC -!- Type 1 RIP subfamily.

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CC EMBL; M34859; AAA34207.1; -.
 CC EMBL; J05434; AAA34206.1; -.
 DR PIR; J70566; RLTZT.
 CC DR PDB; 1G1S; X-ray; A=23-270.
 CC DR PDB; 1J4G; X-ray; A/B/C/D=23-270.
 CC DR PDB; 1MBJ; X-ray; @=24-270.
 CC DR PDB; 1MRK; X-ray; @=24-270.
 DR PRINTS; PRO0275; SHIGA_RICIN; 1.
 DR KW 3D-structure; Antiviral; Direct protein sequencing; Hydrolase;
 KW Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 23
 FT CHAIN 24 270
 PROPEP 271 289
 FT ACT SITE 183 183
 FT CONFLICT 57 60
 FT CONFLICT 82 84
 FT CONFLICT 87 87
 FT CONFLICT 92 92
 FT CONFLICT 143 144
 FT CONFLICT 196 195
 FT CONFLICT 215 216
 FT CONFLICT 231 231
 FT CONFLICT 234 234
 FT CONFLICT 246 266
 FT CONFLICT 247 247
 FT STRAND 25 28
 FT TURN 30 31
 FT HELIX 34 46
 FT TURN 47 47
 FT STRAND 50 54
 FT TURN 55 56
 FT STRAND 57 60
 FT HELIX 66 69
 FT STRAND 70 76
 FT TURN 78 79
 FT STRAND 82 88
 FT TURN 89 92
 FT STRAND 93 99
 FT TURN 100 101
 FT STRAND 102 105
 FT HELIX 109 114
 FT TURN 115 117
 CC TURN 124 127
 FT STRAND 134 141
 FT HELIX 142 142
 FT TURN 145 147
 FT STRAND 150 150
 FT HELIX 152 163
 FT TURN 164 165
 FT HELIX 167 180
 FT TURN 181 181
 FT HELIX 182 186
 FT STRAND 187 187
 FT HELIX 188 195
 FT TURN 196 196
 FT STRAND 202 202
 FT HELIX 206 226
 FT TURN 227 230
 FT STRAND 231 239
 FT TURN 241 242
 FT STRAND 245 250
 FT TURN 251 252
 FT HELIX 254 258
 FT TURN 259 259
 FT STRAND 260 260
 FT STRAND 263 263
 FT TURN 266 268
 FT SEQUENCE 289 AA; 31676 MW; 5C0B0BB630575BB9 CRC64;
 SQ

Query Match 1 99.9%; Score 1429; DB 1; Length 289;
 Best Local Similarity 99.7%; Pred. No. 8.3e-104;
 Matches 288; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MIRFLYVSLLTLTFLTPAVEGDYFRLSGATSSYYGVISNLKALPNERKUDIPLL 60
 Db 1 MIRFLYVSLLTLTFLTPAVEGDYFRLSGATSSYYGVISNLKALPNERKUDIPLL 60
 QY 61 RSSLPGSQRYALIHLTNYADETISVAIDTVNVIYNGYRAGDTSYFNEASATEAKYVFK 120
 Db 61 RSSLPGSQRYALIHLTNYADETISVAIDTVNVIYNGYRAGDTSYFNEASATEAKYVFK 120
 Db 121 DAMRKVTLPSYGNERYLQTAKGKINRIPGIPALDSAITLFLYNNASASALMVLQS 180
 Db 121 DAMRKVTLPSYGNERYLQTAKGKINRIPGIPALDSAITLFLYNNASASALMVLQS 180
 QY 181 TSEARRYKPIFOQIGKRVDKFLPSLAIISLENSNSALSKOIQASTNGOFESPVULIN 240
 Db 181 TSEARRYKPIFOQIGKRVDKFLPSLAIISLENSNSALSKOIQASTNGOFESPVULIN 240
 QY 241 AQNQRTITNDAGVTSNIALLNNNMAAMDDVPMPTOSFGCQSYAL 289
 Db 241 AQNQRTITNDAGVTSNIALLNNNMAAMDDVPMPTOSFGCQSYAL 289

RESULT 2

084SVB
 ID 084SVB
 AC 084SVB;
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Trichosanthin.
 GN Name=RCS;
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxID=3677;
 RN [1]
 SEQUENCE FROM N.A.
 RA Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.

61	RSSLGDSQRVYLAVLTDINABETISVAIDVTSVINGRAGDTSYFNEASATEAKYVK	DB
QY	121 DAMRKVTLPSGNYERLQTAGKIRKENPIGLPALSATLTFYNNANSASALMVLIQS 180	FT
Db	121 DAMRKVTLPSGNYERLQTAGKIRKENPIGLPALSATLTFYNNANSASALMVLIQS 180	FT
QY	181 TSEARKYIEQQGKRVKDFKFLPSLAISSLENSALSAIQIQTASTNNQFESPVVLIN 240	FT
Db	181 TSEARKYIEQQGKRVKDFKFLPSLAISSLENSALSAIQIQTASTNNQFESPVVLIN 240	FT
QY	241 AONQRTITNDAGVTSNIALLNRMAMDDDPVMTQSFGCCSYAI 289	FT
Db	241 AONQRTITNDAGVTSNIALLNRMAMDDDPVMTQSFGCCSYAI 289	FT
RESULT 5		FT
RIPS_TRIKI		CHAIN
ID_RIPS_TRIKI		24
STANDARD;		270
PRT;		C.
289 AA.		Ribosome-inactivating protein Karasurin-
AC		A.
P244_78;		Removed in mature form.
DT	01-MAR-1992 (Rel. 21, Created)	FT
DT	15-DEC-1998 (Rel. 37, Last sequence update)	PROPEP
DT	05-JUL-2004 (Rel. 44, Last annotation update)	ACT SITE
DE	Ribosome-inactivating protein karasurin precursor (EC 3.2.2.22) (rRNA N-glycosidase)	SEQUENCE
OS	Trichosanthes kirilowii (Mongolian snake-gourd).	FT
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.	PROSITE; PS00275; SHIGA_RICN; 1.
OC	NCBI_TaxID=3677;	Antiviral; Direct protein sequencing; Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
RN	[1]	SIGNAL
RP	SEQUENCE FROM N.A.	FT
RC	TRISSUBRoot tuber;	CHAIN
RC	MEDLINE=9735652; PubMed=9212998;	24
RT	Mizukami H., Iida K., Kondo T., Ogihara Y.;	270
RT	"Cloning and bacterial expression of a gene encoding ribosome-inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes kirilowii var. Japonica";	C.
RL	Biol. Pharm. Bull. 20:711-713 (1997).	Ribosome
RN	[2]	inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes kirilowii var. Japonica";
RP	SEQUENCE OF 24-270.	DE
RX	MEDLINE=92005921; PubMed=1914000;	DE
RA	Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;	DE
RT	"The complete amino acid sequence of an abortifacient protein, karasurin."	DE
RL	Chem. Pharm. Bull. 39:1244-1249 (1991).	DE
CC	- - FUNCTION: Abortion-inducing protein. It inactivates eukaryotic 60S ribosomal subunits. Endohydrolysis of the N-glycosidic bond at one	DE
CC	- - CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenine on the 28S rRNA.	DE
CC	- - SIMILARITY: Belongs to the ribosome-inactivating protein family. Type I RIP subfamily.	DE
CC	[1]	DE
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	DE
CC	[2]	DE
RP	SEQUENCE FROM N.A.	DE
RA	Xu L.;	DE
RL	Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.	DE
CC	- - CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenine on the 28S rRNA.	DE
CC	- - SIMILARITY: Belongs to the ribosome-inactivating protein family.	DE
EMBL	U2675; AAN7095.1; -.	EMBL
DR	HSSP; P0989; IMRJ.	DR
DR	InterPro; IPR001574; RIP.	DR
DR	InterPro; IPR001574; RIP.	DR
DR	PRINTS; PR00396; SHIGARICIN.	DR
DR	PROSITE; PS00275; SHIGA_RICN; 1.	DR
KW	Antiviral; Direct protein sequencing; Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.	FT
KW	SIGNAL	FT
FT	POTENTIAL	SEQUENCE
CHAIN	2	270
DR	Ribosome-inactivating protein karasurin-	SQ

Query Match	88.7%	Score 1269; DB 2; Length 270;	Best Local Similarity	95.2%; Pred. No. 2.6e-91;	Matches 257; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
Qy	1	MIRFLVLSSLILTLFLTPAVEGDVSRLSGATSSSYGVFISNLKALPNERKLYDPLL	Qy	121	DAMRKVTPYSGNVERQTAAGKIRENPLGLPALSITTYFYNANSAASALMVLIOS
Db	1	MIRFLVLSSLILTLFLTPAVEGDVSRLSGATSSSYGVFISNLKALPNERKLYDPLL	Db	121	DAMRKVTPYSGNVERQTAAGKIRENPLGLPALSITTYFYNANSAASALMVLIOS
Qy	61	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Qy	181	TSBARYKPIEQDQIGRKVDTKFLPSLALISLENSWALSQIOIASTNGQFESPVVLIN
Db	61	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Db	181	TSBARYKPIEQDQIGRKVDTKFLPSLALISLENSWALSQIOIASTNGQFESPVVLIN
Qy	1	MIRFLVLSSLILTLFLTPAVEGDVSRLSGATSSSYGVFISNLKALPNERKLYDPLL	Qy	121	DAMRKVTPYSGNVERQTAAGKIRENPLGLPALSITTYFYNANSAASALMVLIOS
Db	1	MIRFLVLSSLILTLFLTPAVEGDVSRLSGATSSSYGVFISNLKALPNERKLYDPLL	Db	121	DAMRKVTPYSGNVERQTAAGKIRENPLGLPALSITTYFYNANSAASALMVLIOS
Qy	61	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Qy	181	TSBARYKPIEQDQIGRKVDTKFLPSLALISLENSWALSQIOIASTNGQFESPVVLIN
Db	61	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Db	181	TSBARYKPIEQDQIGRKVDTKFLPSLALISLENSWALSQIOIASTNGQFESPVVLIN
Qy	121	DAMRKVTPYSGNVERQTAAGKIRENPLGLPALSITTYFYNANSAASALMVLIOS	Qy	121	DAMRKVTPYSGNVERQTAAGKIRENPLGLPALSITTYFYNANSAASALMVLIOS
Db	121	DAMRKVTPYSGNVERQTAAGKIRENPLGLPALSITTYFYNANSAASALMVLIOS	Db	121	DAMRKVTPYSGNVERQTAAGKIRENPLGLPALSITTYFYNANSAASALMVLIOS
Qy	181	TSBARYKPIEQDQIGRKVDTKFLPSLALISLENSWALSQIOIASTNGQFESPVVLIN	Qy	181	TSBARYKPIEQDQIGRKVDTKFLPSLALISLENSWALSQIOIASTNGQFESPVVLIN
Db	181	TSBARYKPIEQDQIGRKVDTKFLPSLALISLENSWALSQIOIASTNGQFESPVVLIN	Db	181	TSBARYKPIEQDQIGRKVDTKFLPSLALISLENSWALSQIOIASTNGQFESPVVLIN
Qy	241	AQNQRTITNDAGWTSNIALLNRMNA 270	Qy	241	AQNQRTITNDAGWTSNIALLNRMNA 270
Db	241	AQNQRTITNDAGWTSNIALLNRMNA 270	Db	241	AQNQRTITNDAGWTSNIALLNRMNA 270
RESULT 7			RESULT 8		
Q6PRG5			Q8LPV7		
ID	Q6PRG5	PRELIMINARY;	ID	Q8LPV7	PRELIMINARY;
AC	Q6PRG5;	PRT;	AC	Q8LPV7;	PRT;
DT	05-JUL-2004 (TREMBLRE, 27, Created)	270 AA.	DT	01-OCT-2002 (TREMBLRE, 22, Created)	270 AA.
DT	05-JUL-2004 (TREMBLRE, 27, Last sequence update)		DT	01-OCT-2002 (TREMBLRE, 22, Last sequence update)	
DE	Trichomisin (Fragment).		DT	01-OCT-2003 (TREMBLRE, 25, Last annotation update)	
GN	Name=tcm;		DE	Trichosanthin precursor (Fragment).	
OS	Trichoranthus kirilowii (Mongolian snake-gourd).		GN	Name=tcs;	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.		OS	Trichoranthus kirilowii (Mongolian snake-gourd).	
OC			OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.	
OX			OC		
RN	[1]		RN		
RP	SEQUENCE FROM N.A.		RP	SEQUENCE FROM N.A.	
RA	Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.,		RA	Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.,	
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
-I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one			-I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one		
CC	specific adenosine on the 28S rRNA.		CC	specific adenosine on the 28S rRNA.	
-I- SIMILARITY: Belongs to the ribosome-inactivating protein family.			-I- SIMILARITY: Belongs to the ribosome-inactivating protein family.		
DR	EMBL: AY082348; AAC2782.1; -.		DR	EMBL: AY082348; AAC2782.1; -.	
DR	PTR; JG0502; JG0532.		DR	HSP; P09989; IMKJ.	
DR	GO; GO-0016787; F:hydrolase activity; IEA.		DR	GO; GO-0016787; F:hydrolase activity; IEA.	
DR	GO; GO-0030598; F:RNA N-glycosidase activity; IEA.		DR	GO; GO-0030598; F:RNA N-glycosidase activity; IEA.	
DR	GO; GO-006552; P:defense response; IEA.		DR	GO; GO-006552; P:defense response; IEA.	
DR	PRION; PR00161; RIP; 1.		DR	PRION; PR00161; RIP; 1.	
DR	PROSITE; PS0275; SHIGA_RICIN.		DR	PROSITE; PS0275; SHIGA_RICIN.	
FT	Hydroxylase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.		FT	Hydroxylase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.	
FT	PROSITE; PS0275; SHIGA_RICIN; 1.		FT	PROSITE; PS0275; SHIGA_RICIN; 1.	
FT	Signal		FT	Signal	
FT	1		FT	1	
FT	23		FT	23	
FT	24		FT	24	
FT	>270		FT	>270	
NON_TER			NON_TER		
SEQUENCE	270 AA; 29683 MW; 53173B754P9B769 CRC64;		SEQUENCE	270 AA; 29683 MW; 53173B754P9B769 CRC64;	
Query Match	88.1%	Score 1260; DB 2; length 270;	Query Match	88.1%	Score 1260; DB 2; length 270;
Best Local Similarity	95.2%; Pred. No. 1.3e-90;	Best Local Similarity	95.2%; Pred. No. 1.3e-90;	Best Local Similarity	95.2%; Pred. No. 1.3e-90;
Matches	257; Conservative 5; Mismatches 8; Indels 0; Gaps 0;	Matches	257; Conservative 5; Mismatches 8; Indels 0; Gaps 0;	Matches	257; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
FT			FT		
SEQUENCE	270 AA; 29649 MW; SBB513B754P9B769 CRC64;		SEQUENCE	270 AA; 29649 MW; SBB513B754P9B769 CRC64;	
Query Match	88.3%; Score 1264; DB 2; Length 270;	Query Match	88.1%; Score 1260; DB 2; length 270;	Query Match	88.1%; Score 1260; DB 2; length 270;
Best Local Similarity	95.6%; Pred. No. 6.4e-91;	Best Local Similarity	95.6%; Pred. No. 6.4e-91;	Best Local Similarity	95.6%; Pred. No. 1.3e-90;
Matches	258; Conservative 5; Mismatches 7; Indels 0; Gaps 0;	Matches	258; Conservative 5; Mismatches 7; Indels 0; Gaps 0;	Matches	258; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
FT			FT		
SEQUENCE	270 AA; 29649 MW; SBB513B754P9B769 CRC64;		SEQUENCE	270 AA; 29649 MW; SBB513B754P9B769 CRC64;	
Qy	1	MIRFLVLSSLILTLFLTPAVEGDVSRLSGATSSSYGVFISNLKALPNERKLYDPLL	Qy	1	MIRFLVLSSLILTLFLTPAVEGDVSRLSGATSSSYGVFISNLKALPNERKLYDPLL
Db	1	MIRFLVLSSLILTLFLTPAVEGDVSRLSGATSSSYGVFISNLKALPNERKLYDPLL	Db	1	MIRFLVLSSLILTLFLTPAVEGDVSRLSGATSSSYGVFISNLKALPNERKLYDPLL
Qy	61	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Qy	181	TSBARYKPIEQDQIGRKVDTKFLPSLALISLENSWALSQIOIASTNGQFESPVVLIN
Db	61	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Db	181	TSBARYKPIEQDQIGRKVDTKFLPSLALISLENSWALSQIOIASTNGQFESPVVLIN
Qy	120	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Qy	120	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Db	120	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Db	120	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Qy	180	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Qy	180	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Db	180	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Db	180	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Qy	240	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Qy	240	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Db	240	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Db	240	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Qy	270	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Qy	270	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Db	270	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Db	270	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Qy	296	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Qy	296	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Db	296	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Db	296	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Qy	29683	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Qy	29683	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Db	29683	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Db	29683	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Qy	53173B754P9B769	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Qy	53173B754P9B769	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Db	53173B754P9B769	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Db	53173B754P9B769	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Qy	CRC64	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Qy	CRC64	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK
Db	CRC64	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK	Db	CRC64	RSSPGSQRYALHTNAYDETISVALIDTNTVYIMGRAGDTSYFFNEASATEAKYVFK

RC TISSUE=Leaf; MEDLINE=97228081; PubMed=9115985; DOI=10.1021/bi962474+; RA Gawlik S.L., Neubauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M., Siegall C.B.; "Molecular, biological, and preliminary structural analysis of recombinant bryodin 1, a ribosome-inactivating protein from the plant Bryonia dioica.;" Biochemistry 36:3095-3103 (1997). [2]

RL patient number US554110, 30-JUL-1996. [3]

RP SEQUENCE FROM N A. [4]

RA Siegall C.B.; "Cloning and expression of a gene encoding bryodin 1 from Bryonia dioica.;" patent number US554110, 30-JUL-1996. [3]

RN SEQUENCE OF 24-66. [4]

RC TISSUE=Seed; MEDLINE=89126691; PubMed=2753596; RA Montecuccchi P.C., Lazarini A.M., Barbieri L., Stirpe F., Soria M., Lappi D.; "N-terminal sequence of some ribosome-inactivating proteins.;" Int. J. Pept. Protein Res. 33:263-267(1989). [4]

RN SEQUENCE OF 24-43. [4]

RC TISSUE=Root; MEDLINE=9551812; PubMed=7849072; RA Siegall C.B., Gawlik S.L., Chace D., Wolff E.A., Mixan B., Marquardt H.; "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunocomjugates.;" Bioconjug. Chem. 5:423-429(1994).

CC -!- FUNCTION: Ribosome-inactivating protein of type 1, inhibits protein synthesis in animal cells.

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenine on the 28S rRNA.

CC -!- PWT: Appears to undergo proteolytic cleavage in the C-terminal to produce a shorter protein.

CC -!- BIOTECHNOLOGY: Especially useful as immunotoxin for pharmaceutical applications as it has low toxicity in rats and mice but is potent once inside target cells.

CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family. Type 1 RIP subfamily.

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CC -----

CC EMBL; 124020; -; NOT_ANNOTATED_CDS.

DR PIR; S16491; S16491; PDB; 1BRY; X-ray; Y/Z=23-270. InterPro; IPR01574; RIP. Pfam; PF00161; RIP_1. PRINTS; PRO0396; SHIGARICIN.

DR PROSITE; PS00215; SHIGARICIN_1. 3D-STRUCTURE; Direct protein sequencing; Glycoprotein; Hydrolase; KW 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase; KW Multigene family; Plant defense; Protein synthesis inhibitor; Signal; Toxin.

FT SIGNAL 1 23 FT CHAIN 24 270 FT PROPEP 271 290 FT ACT SITE 183 183 FT ACT SITE 212 212 FT CARBOHYD 214 214 FT CARBOHYD 250 250 FT MUTAGEN 212 212 FT CONFLICT 61 65 FT STRAND 25 28 FT TURN 30 31

FT TURN 47 47 FT STRAND 50 54 FT TURN 55 56 FT STRAND 57 60 FT HELIX 66 69 FT STRAND 70 76 FT TURN 78 79 FT STRAND 82 88 FT TURN 89 92 FT STRAND 93 99 FT TURN 100 101 FT STRAND 102 105 FT HELIX 109 114 FT TURN 115 117 FT STRAND 120 121 FT TURN 124 127 FT HELIX 134 141 FT TURN 142 142 FT STRAND 145 147 FT HELIX 150 150 FT TURN 152 153 FT STRAND 155 155 FT TURN 164 165 FT HELIX 167 186 FT TURN 187 187 FT STRAND 188 196 FT TURN 202 202 FT HELIX 206 213 FT TURN 214 214 FT HELIX 215 225 FT TURN 226 230 FT STRAND 231 239 FT TURN 241 242 FT STRAND 245 250 FT TURN 251 252 FT HELIX 254 257 FT TURN 258 259 FT STRAND 260 250 FT STRAND 263 253 FT HELIX 266 253

FT SEQUENCE 290 AA; 31788 MW; E966CD9C031A42DB CRC64;

Query Match Best Local Similarity 81.9%; Score 1171.5; DB 1; Length 290; Matches 236; Conservative 26; Mismatches 27; Indels 1; Gaps 1; QY 1 MRFPLVSLSLITLFLPTPAVGQDVSLRSGTSSYGVFSNLKALPNERKLYDPLL 60 Db 1 MIKLVVWLLWLLFLKSKPTVCDVSLRSLGATTSQVFLKMLREALPYERKVNTPLL 60 QY 61 RSSLPGSORYALIHLTNYADETSIVADLVTNYIMGRAGDTSYFFNEASATEAKYVK 120 Db 61 RSLISGSRVTLHLHNVADETISVAUDVNTNYIMGLADSYFFNEASATEAKYVK 120 Db 121 DAMKVUTLPSYSENVERLQTAAGSKIRENIPLGIPALDAISITTYFYNANSAAALMVLTOS 180 Db 121 DAKKKVVLPSYSENVERLQTAAGSKIRENIPLGIPALDAISITTYFYNANSAAALMVLTOS 180 QY 181 TEAARYKTFEDQIGKVKDFTLPSLAIISLNSWSLSKQIASTNGQESPVULIN 240 Db 181 TEAARYKTFEDQIGKVKDFTLPSLAIISLNSWSLSKQIASTNGQESPVULIN 240 QY 241 AQNQRVITINVDAGVTSNIALLNRNMMAMDDDVPMTO-SFGCGSYAL 289 Db 241 GHNQRVTSITNASARVWNSNIALLNRNNTAAGEDISMTLIGFENHGLYI 290

RESULT 12 RPL1_MONCH ID RPL1_MONCH STANDARD; PRT; 286 AA. AC P16094; P24697; DT 01-APR-1990 (Rel. 14, Created) DT 01-MAR-1992 (Rel. 21, Last sequence update)

DE 25-OCT-2004 (Rel. 45. Last annotation update) (tRNA
 DE Ribosome-inactivating protein momordin I precursor (EC 3.2.2.22) (tRNA
 DE N-glycosidase) (Alpha-momorcharin) (Alpha-MC1C).
 OS Momordica charantia (bitter gourd) (Balsam pear).
 OC Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyt; Magnoliophyt; eudicotyledons; core eudicots; rosids;
 OC eurrosids I; Cucurbitales; Cucurbitaceae; Momordica.
 OC NBI_TaxID=5673;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Seed;
 RX MEDLINE:9119486; PubMed=2001404; DOI=10.1016/0167-4781(91)90070-3;
 RA HO W.K.K., Liu S.C., Shaw P.C., Yeung H.W., NG T.B., Chan W.Y.;
 RT "Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating
 protein";
 RL Biochim. Biophys. Acta 1088:311-314(1991).
 RN [2]
 RP SEQUENCE OF 24-38.
 RC TISSUE-Seed;
 RX MEDLINE:8918326691; PubMed=2753596;
 RA Montecuccchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
 Lappi D.;
 RT "N-terminal sequence of some ribosome-inactivating proteins.";
 RL Int. J. Pept. Protein Res. 33:263-267(1989).
 RN [31]
 RP SEQUENCE OF 24-70.
 RC TISSUE-Seed;
 RX MEDLINE:89005108; PubMed=3262509;
 RA Ceballos P., Dubossoy D., Falaschi A.I., Barbieri L., Guillenot J.C.,
 Ferrara P., Bollosoy A., Canini P., Stirpe F.;
 RT "Trichosanthin, a ribosome-inactivating protein from the seeds of
 Trichosanthes kirilowii Maximowicz. Purification, partial
 characterization and use for preparation of immunotoxins.";
 RL Eur. J. Biochem. 176:561-588(1988).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE:9435547; PubMed=8075985;
 RA Ren J., Wang Y., Dong Y., Stuart D.I.;
 RT "The N-glycosidase mechanism of ribosome-inactivating proteins implied
 by crystal structures of alpha-momorcharin.";
 RL Structure 2:7-16(1994).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.16 ANGSTROMS).
 RX MEDLINE:9419822; PubMed=8143869; DOI=10.1016/0014-5793(94)80491-5;
 RA Huang J., Tickle I.J., Wood S.P.;
 RT "Crystal structure of momordin, a type I ribosome inactivating protein
 from the seeds of Momordica charantia.";
 RL FEBS Lett. 342:154-158(1994).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE:95344383; PubMed=7619070;
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
 RT "Studies on crystal structures, active-centre geometry and
 depurinating mechanism of two ribosome-inactivating proteins.";
 RL Biochem. J. 309:285-290(1995).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenine on the 28S rRNA.
 CC -!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC Type 1 RNP subfamily.
 CC
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 CC
 DR EMBL; X57682; CAA40869.1; -.
 DR PIR; S14273; RUPUCG.
 DR PDB; 1ABA; X-ray; @=24-269.
 DR PDB; 1AAB; X-ray; @=24-269.
 DR PDB; 1AIC; X-ray; @=24-269.

DR	PDB; 1F8Q; X-ray; A-24-286.
DR	IMOM; X-ray; @=24-269.
DR	IMRG; X-ray; @=24-286.
DR	IMRH; X-ray; @=24-286.
DR	PDB; IMRI; X-ray; @=24-286.
DR	Glycosuitedb; P16094; -.
DR	Interpro; IPR01574; RIP.
DR	PRINTS; PRO0161; RIP; 1.
DR	PROSITE; PS00275; SHIGARICIN.
KW	3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
FT	SIGNAL 1 23
FT	CHAIN 24 269
FT	PROPEP 270 286
FT	ACT SITE 183 183
FT	CARBOHYD 250 250
FT	STRAND 25 28
FT	HELIX 34 47
FT	STRAND 50 54
FT	TURN 55 56
FT	STRAND 57 60
FT	HELIX 66 69
FT	STRAND 70 76
FT	TURN 78 79
FT	STRAND 82 88
FT	TURN 89 92
FT	STRAND 93 99
FT	TURN 100 101
FT	STRAND 102 105
FT	HELIX 109 114
FT	TURN 115 117
FT	TURN 120 121
FT	STRAND 124 127
FT	HELIX 134 141
FT	HELIX 145 147
FT	STRAND 150 150
FT	HELIX 152 162
FT	TURN 163 163
FT	STRAND 167 186
FT	HELIX 187 187
FT	HELIX 188 195
FT	TURN 196 197
FT	STRAND 202 202
FT	HELIX 206 225
FT	TURN 226 230
FT	STRAND 231 238
FT	TURN 240 241
FT	STRAND 246 250
FT	TURN 251 252
FT	HELIX 254 258
FT	TURN 259 259
FT	STRAND 260 260
FT	STRAND 263 263
FT	HELIX 266 268
SQ	SEQUENCE 286 AA; 31532 MW; B1B013ABEBC216CP CRC64;
Query	Best Local Similarity 60.6%; Score 866.5; DB 1; Length 286; Matches 179; Conservative 40; Mismatches 63; Indels 1; Gaps 1;
Qy	1 MIRPLVLSLILTLPLTIPAVEGDSFRISGATSSSYGVFISNLKALPNERKLYDPLL 60 1 : : : : : : : : 1 MSRFSPVSLFLIAIFLIGLSIVKVDGVSFLGSPRSGMFIKDLRNALPFRKVYNIPLL 60
Qy	61 RSSLPGSGORYALIHLNWADETISVAIDTVNTVYIMGYRAGDTSYFFNEASATEAKYVFK 120 : : : : : : : : : : : : : : : 61 LPSVSGAGRYLLMLHFNFDGKTTIVAVDVTNVYIMGYLADTSYFFNEPAMELASQYVFR 120
Db	121 DAMRKVTLPLPSGYVERIOTAAKGIRENIPGLPALSAITLTFYVNTNSASALMVLQS 180 : : : : : : : : : : : : : : : 121 DARRKITPLPSGYTERIQLAAGSKPERKIPGLPALSIASTLRLDMSDTAAAGALLQIT 180

Qy	180	SISSEAAKPKFIEQIGKGVKDTPSLATLISLNSALSKOIQIASTNGQFESPVLI	239	CC	HIV-1 integrase, irreversibly relax supercoiled DNA and catalyzes double-stranded breakage. Acts also as a ribosome inactivating protein.
Db	178	TTABASFRKYIEQGQTRIPKNEVSPASLNEWSLKOIQIASTNGAFRTPVII	237	CC	-I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenine on the 28S rRNA.
Qy	240	NAQNQRVITNTDAGVTSNIALLNRMAMDDPVS	277	CC	-I- PDB: Bound to a branched hexariboside.
Db	238	DNKGQRVIEKKVNVKVNNTKUILLNKQNIAAFDDGIP	275	CC	-I- MISCELLANEOUS: Manganese or zinc required for enhancing substrate binding rather than catalysis.
RESULT 15				CC	-I- MISCELLANEOUS: The oligosaccharide does not play a role in the polypeptide chain and probably does not play a role in the enzymatic function.
RIP3_MOMCH				CC	-I- MISCELLANEOUS: Is not toxic to uninfected normal cells as it cannot enter into them.
AC	P24817; Q41257; Q9P8H2; Q9TUV7;			CC	-I- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DT	01-MAR-1992 (Rel. 2.1, Created)			CC	Type 1 RIP subfamily.
DT	03-JUL-2004 (Rel. 4.4, Last sequence update)			CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DB	25-OCT-2004 (Rel. 4.5, Last annotation update)			CC	-----
DE	Ribosome-inactivating protein beta-momorcharin precursor (EC 3.2.2.22)			CC	-----
DE	RNA N-glycosidase (MAP30) (B-MMC)			CC	-----
GN	Name=MAP30; Synonyms=RIP;			CC	-----
OS	Monordica charantia (Bitter gourd) (Balsam pear).			CC	-----
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			CC	-----
OC	Spermatophyta; Magnoliophyta; eudicots; rosids;			CC	-----
OC	eurosid I; Cucurbitales; Cucurbitaceae; Momordica.			CC	-----
OX	NCBI_TAXID=5673;			CC	-----
RN	[1]			CC	-----
RP	SEQUENCE FROM N.A., AND FUNCTION.			DR	DR: S79450; AAB35194.2; --.
RC	TISSUE=Leaf;			DR	EMBL: AR28481; ARG33028.1; --.
RX	MEDLINE=95344347; PubMed=665070; DOI=10.1016/0378-1119(95)00186-A;			DR	EMBL: AY523412; AAS17014.1; --.
RA	Lee-Huang S., Huang P.L., Chen H.-C., Huang P.L., Bourinbaiar A.,			DR	EMBL: AJ234541; CAC08217.1; --.
RA	Huang H.-I., Kung H.-F.;			DR	PIR: B61318; B61318.
RT	"Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter melon."			DR	PIR; JC4235; JC4235.
RT	Gene 161:151-156(1995).			DR	PDB: 1CP5; X-ray; A=B=.
RN	[2]			DR	PDB: 1D8V; NMR; A=.
RP	SEQUENCE FROM N.A.			DR	DR: InterPro; IPR001574; RIP.
RA	Quanhong Y., Rike P., Aisheng X.,			DR	Pfam: PF00161; RIP; 1.
RN	Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.			DR	PRINTS; PRO0396; SHIGARICIN.
RP	SEQUENCE OF 23-286 FROM N.A.			DR	PROSITE; PS00215; SHIGA RICIN; 1.
RA	Wei Y.-P., Cai L.-B., Zhuang W.;			DR	KW: 3D-structure; Antiviral; Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
RT	"Cloning, rip gene and identification of its resistance to Aspergillus flavus."			FT	FT: SIGNAL_1
RT	Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.			FT	FT: CHAIN_24
RN	[4]			FT	FT: ACT_SITE_93
RP	SEQUENCE OF 23-286 FROM N.A.			FT	FT: ACT_SITE_132
RA	Nguyen Huy H., Nghiem Ngoc M., Dao Huy P., Le Tran B., Nong Van H.;			FT	FT: ACT_SITE_181
RT	"Expression of a RIP gene from Monordica charantia in E. coli."			FT	FT: ACT_SITE_184
RL	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.			FT	FT: CARBONYD_74
RN	[5]			FT	FT: CONFLICT_23
RP	SEQUENCE OF 24-67.			FT	FT: CONFLICT_37
RC	TISSUE=Seed;			FT	FT: CONFLICT_67
RX	MEDLINE=91032105; PubMed=1699801; DOI=10.1016/0014-5793(90)80438-0;			FT	FT: CONFLICT_67
RA	Lee-Huang S., Huang P.L., Nara P.L., Chen H.-C., Kung H.-F., Huang P.,			FT	FT: CONFLICT_147
RA	Huang H.-I., Huang P.L.;			FT	FT: CONFLICT_147
RT	"MAP 30: a new inhibitor of HIV-1 infection and replication."			FT	FT: CONFLICT_188
RL	FEBS Lett. 272:12-18(1990).			FT	FT: CONFLICT_228
RN	[6]			FT	FT: CONFLICT_228
RP	STRUCTURE BY NMR OF 24-286, AND DNA BINDING.			FT	FT: CONFLICT_228
RX	Pubmed=0571185; DOI=10.1016/S0092-8674(00)81529-9;			FT	FT: CONFLICT_228
RA	Wang Y.-X., Neamati N., Jacob J., Palmer I., Stahl S.J., Kaufman J.D.,			FT	FT: CONFLICT_228
RA	Ruang P.L., Huang P.L., Winslow H.E., Pommier Y., Wingfield P.T.,			FT	FT: CONFLICT_228
RA	Huang P.L., Huang P.L., Winslow H.E., Pommier Y., Wingfield P.T.,			FT	FT: CONFLICT_228
RA	Bax A., Torchia D.A., Pommier Y., Wingfield P.T.,			FT	FT: CONFLICT_228
RT	"Solution structure of anti-HIV-1 and anti-tumor protein MAP30: structural insights into its multiple functions."			FT	FT: CONFLICT_228
RL	Cell 99:433-442(1999).			FT	FT: CONFLICT_228
RN	[7]			FT	FT: CONFLICT_228
RP	X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 24-272.			FT	FT: CONFLICT_228
RX	Pubmed=1329776; DOI=10.1107/S00744990032977;			FT	FT: CONFLICT_228
RA	Yuan Y.-R., He Y.-N., Xiong J.-P., Xia Z.-X.;			FT	FT: CONFLICT_228
RT	"Three-dimensional structure of beta-momorcharin at 2.55 A resolution."			FT	FT: CONFLICT_228
RL	Acta Crystallogr. D 55:1144-1151(1999).			FT	FT: CONFLICT_228
CC	-I- FUNCTION: Possesses anti-HIV and anti-tumor activities. Inhibits			FT	FT: CONFLICT_228

Wed Apr 13 09:27:10 2005

us-09-905-247a-1.rup

Page 11

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:
Db 239 PTGERFQVINVDSDVVKGNIKLILN 263

Search completed: April 12, 2005, 15:13:58
Job time : 127.09 secs

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OM protein - protein search, using sw model																		
Run on: April 12, 2005, 15:05:22 ; Search time 37.2034 Seconds																		
(without alignments)																		
579.883 Million cell updates/sec																		
Title: US-09-905-247A-1	Scoring table: BIOSUM62	Sequence: 1 MIREVVISLLIITLETTPA.....AAMDDDVPMKIQSEGGSVAL 289	Searched: 513545 seqs, 74649064 residues	Total number of hits satisfying chosen parameters: 513545	Minimum DB seq length: 0	Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Alignments										
Database :	Issued Patents AA: * /cgn2_6/ptodata/1/iaa/5A_COMB.pep: * 1: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: * 2: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: * 3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: * 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: * 5: /cgn2_6/ptodata/1/iaa/backfilest1.pep: * 6: /cgn2_6/ptodata/1/iaa/backfilest1.pep: *																	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.																		
SUMMARIES																		
Result No.	Score	Query Length	DB ID	Description														
1	1420	99.2	289	1 US-07-923-692C-4	RESULT 1 US-07-923-692C-4 Sequence 4, Application US/07923692C Patent No. 5316931													
2	1420	99.2	289	1 US-07-923-692C-4	GENERAL INFORMATION:													
3	1420	99.2	289	2 US-08-482-920-4	APPLICANT: Dawson, Jon													
4	1420	99.2	289	3 US-08-484-341-4	APPLICANT: Grantham, George L.													
5	1420	99.2	289	4 US-08-483-502-4	APPLICANT: Turpen, Thomas H.													
6	1420	99.2	289	4 US-09-726-651A-4	APPLICANT: Turpen, Ann Myers													
7	1328	92.8	267	1 US-08-378-761A-7A	APPLICANT: Garger, Stephen J.													
8	1328	92.8	267	1 US-08-485-286-7A	APPLICANT: Grill, Laurence K.													
9	1209	84.5	247	1 US-08-480-113B-6	TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACID													
10	1209	84.5	247	1 US-08-477-484B-6	NUMBER OF SEQUENCES: 11													
11	1209	84.5	247	2 US-08-46-360-6	CORRESPONDENCE ADDRESS:													
12	1209	84.5	247	3 US-08-183-765-6	ADDRESSE: Limbach & Limbach													
13	1209	84.5	247	3 US-09-156-389-6	STREET: 2001 Ferry Building													
14	1209	84.5	247	3 US-09-610-838-6	CITY: San Francisco													
15	1209	84.5	247	4 US-09-711-485-6	STATE: CAL													
16	1209	81.9	290	1 US-08-245-754A-2	ZIP: 94111													
17	1209	81.9	290	2 US-08-907-731-2	COMPUTER READABLE FORM:													
18	1137	79.5	255	1 US-07-901-707-6	MEDIUM TYPE: Floppy disk													
19	1137	79.5	255	1 US-07-980-430-6	COMPUTER: IBM PC compatible													
20	1137	79.5	255	1 US-07-925-336-6	OPERATING SYSTEM: PC-DOS/MS-DOS													
21	1137	79.5	255	5 PCT-US92-09487-6	SOFTWARE: Patent in Release #1.0, Version #1.25													
22	1081	75.5	496	3 US-08-902-486-7	CURRENT APPLICATION DATA:													
23	1071	74.8	248	3 US-08-902-486-7	APPLICATION NUMBER: US 641,617													
24	813.5	56.8	263	1 US-07-901-707-7	FILING DATE: 16-JUN-1991													
25	813.5	56.8	263	1 US-07-980-430-7	PRIOR APPLICATION DATA:													
26	813.5	56.8	263	1 US-08-425-336-7	APPLICATION NUMBER: US 310,881													
27	813.5	56.8	263	1 US-08-480-113B-7	FILING DATE: 22-OCT-1990													
					PRIOR APPLICATION DATA:													
					APPLICATION NUMBER: US 160,771													
					FILING DATE: 26-FEB-1988													
					FILING DATE: 26-FEB-1988													
					PRIOR APPLICATION DATA:													
					APPLICATION NUMBER: US 160,771													
					FILING DATE: 26-FEB-1988													
					PRIOR APPLICATION DATA:													
					APPLICATION NUMBER: US 347,637													
					FILING DATE: 05-MAY-1989													
					PRIOR APPLICATION DATA:													
					APPLICATION NUMBER: US 363,138													
					FILING DATE: 08-JUN-1989													

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 219,279
 FILING DATE: 15-JUL-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Halluin, Albert P.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: BIOG-20121
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-433-4150
 TELEFAX: 415-433-8716
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 289 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-923-692C-4

Query Match 99.2%; Score 1420; DB 1; Length 289;

Best Local Similarity 99.0%; Pred. No. 9.3e-138; Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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 Db 1 MIRFLVISLILTLFLTPAVEGDVSFRLSGATSSSYGVFISNLKALPNERKLYDPLL 60
 QY 61 RSSLPGSQRYALIHLTNYADETISVAIDVTVNYIMGYRAGDTSYFNEASATEAKYVFK 120
 Db 61 RSSLPGSQRYALIHLTNYADETISVAIDVTVNYIMGYRAGDTSYFNEASATEAKYVFK 120
 QY 121 DAMRKVTLPSGNYERLQTAGKIRENPLGLPALSATLTFYNNASASALMVLQS 180
 Db 121 DAMRKVTLPSGNYERLQTAGKIRENPLGLPALSATLTFYNNASASALMVLQS 180
 QY 181 TSEAARYKTFIQQIGKRVDKFLPSLAIISLENSWALSQIQIASTNGQFESPVULIN 240
 Db 181 TSEAARYKTFIQQIGKRVDKFLPSLAIISLENSWALSQIQIASTNGQFESPVULIN 240
 QY 241 AONQRTITNDAGVVTNTAIIINRNMAAMDDVPTQSGCGSYAL 289
 Db 241 AONQRTITNDAGVVTNTAIIINRNMAAMDDVPTQSGCGSYAL 289

RESULT 2
 US-08-184-237-4 Application US/08184237
 ; Patent No. 5583367

GENERAL INFORMATION:
 ; APPLICANT: Donsen, Jon
 ; APPLICANT: Dawson, William O.
 ; APPLICANT: Grantham, George L.
 ; APPLICANT: Turpen, Thomas H.
 ; APPLICANT: Turpen, Ann Myers
 ; APPLICANT: Garren, Stephen J.
 ; APPLICANT: Grill, Laurence K.
 ; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
 ; NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Limbach & Limbach
 ; STREET: 2001 Ferry Building
 ; CITY: San Francisco
 ; STATE: CAL
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/184,237
 ; FILING DATE:
 ; CLASSIFICATION: 435

RESULT 3
 US-08-482-920-4

SEQUENCE 4, Application US/08482920
 ; Patent No. 5866785

RESULT 3
 US-08-482-920-4

SEQUENCE 4, Application US/08482920
 ; Patent No. 5866785

RESULT 3
 US-08-482-920-4

SEQUENCE 4, Application US/08482920
 ; Patent No. 5866785

;

GENERAL INFORMATION:
 ; APPLICANT: Donsen, Jon

APPLICANT: Dawson, William O.
 APPLICANT: Grantham, George L.
 APPLICANT: Turpen, Ann Myers
 APPLICANT: Garger, Stephen J.
 APPLICANT: Grill, Laurence K.
 TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS.
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penne & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,920
 FILING DATE: 07-JUNE-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 184,237
 FILING DATE: 19-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 600,244
 FILING DATE: 22-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 641,617
 FILING DATE: 16-JAN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 310,881
 FILING DATE: 17-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160,766
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160,771
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 347,637
 FILING DATE: 05-MAY-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 363,138
 FILING DATE: 08-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 219,279
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-3660
 TELEFAX: 415-854-3694
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 289 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-482,920-4

RESULT 4 ; Sequence 4, Application US/08484341
 GENERAL INFORMATION:
 APPLICANT: Dawson, Jon
 APPLICANT: Dawson, William O.
 APPLICANT: Grantham, George L.
 APPLICANT: Turpen, Thomas H.
 APPLICANT: Garger, Stephen J.
 TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Limbach & Limbach
 STREET: 2001 Ferry Building
 CITY: San Francisco
 STATE: CAL
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,341
 FILING DATE: 07-Jun-1995
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/184,237
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 600,244
 FILING DATE: 22-OCT-1990
 APPLICATION NUMBER: US 641,617
 FILING DATE: 16-JAN-1991
 APPLICATION NUMBER: US 310,881
 FILING DATE: 17-FEB-1989
 APPLICATION NUMBER: US 160,766
 FILING DATE: 26-FEB-1988
 APPLICATION NUMBER: US 160,771
 FILING DATE: 26-FEB-1988
 APPLICATION NUMBER: US 347,637
 FILING DATE: 05-MAY-1989
 APPLICATION NUMBER: US 363,138
 FILING DATE: 08-JUN-1989
 APPLICATION NUMBER: US 219,279
 FILING DATE: 15-JUL-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Halluin, Albert P.
 REFERENCE/DOCKET NUMBER: B10G-20121 USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-433-4150
 TELEFAX: 415-433-8716
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 289 amino acids

61 RSSLPGSQRVALHLTVADETISVAIDVTVNVIMGYRAGDTSYFFNEASATEAKVFK 120
 121 DAMRKVTLPSGYNERQTAAGKIRENPLGIPALDSSATTLYNNANSASALMILQS 180
 121 DAMRKVTLPSGYNERQTAAGKIRENPLGIPALDSSATTLYNNANSASALMILQS 180
 181 TSEARRYKIEQIGKRVDTKFLPSLAIISLENSWSALKQTOIASTNGOPESPVLIN 240
 181 TSEARRYKIEQIGKRVDTKFLPSLAIISLENSWSALKQTOIASTNGOPESPVLIN 240
 QY 241 ADQRVITNUAGWVNTIAJLNRNMAANDDVNTQSGCGSIAL 289
 Db 241 AQNRVWNTVNDAGWVNTIAJLNRNMAANDDVNTQSGCGSYAI 289

Query Match 99.2%; Score 1420; DB 3; Length 289;
 Best Local Similarity 99.0%; Pred. No. 9.3e-138; Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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 Db 1 MIRFLVLSSLILTLTTPAVEGDSFRUSGATSSSYGVISNRKALPNERKUDIPLL 60

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 Db 61 RSSLPGSQRVALIHLTNAYDETSVAIDVINVYMGYRAGDTSYFNEASATEAKYVK 120

Query 121 DAMKVTLPYSGNVERLQTAGKIRENTIPLGLPALSATIITLEFVNNSASAALMVLQS 180
 Db 121 DAMKVTLPYSGNVERLQTAGKIRENTIPLGLPALSATIITLEFVNNSASAALMVLQS 180

Query 181 TSEARYKPFEOQIGKRVDTKFLPLSALISLENSWALSALSQIQIQTASTNGQFEPVVLIN 289
 Db 181 TSEARYKPFEOQIGKRVDTKFLPLSALISLENSWALSALSQIQIQTASTNGQFEPVVLIN 240

Query 241 AQNQRTITNDAGVTSNIALLNRNNMAMDDDPVMTQSFGCGSYAI 289
 Db 241 AQNQRTITNDAGVTSNIALLNRNNMAMDDDPVMTQSFGCGSYAI 289

RESULT 5
 US-08-483-502-4

Sequence 4, Application US/08483502
 Patent No. 628492
 GENERAL INFORMATION:
 APPLICANT: Donson, Jon
 APPLICANT: Dawson, William O.
 APPLICANT: Grantham, George L.
 APPLICANT: Turpen, Thomas H.
 APPLICANT: Turpen, Ann Myers
 APPLICANT: Grill, Laurence K.
 TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
 NUMBER OF SEQUNECES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue N.W., Suite 1000
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,502
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/39,143
 FILING DATE:
 APPLICATION NUMBER: US 600,244
 FILING DATE: 22-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 641,617
 FILING DATE: 16-JAN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 310,881
 FILING DATE: 17-FEB-1989
 PRIOR APPLICATION DATA:

RESULT 6
 US-09-726-651A-4

Sequence 4, Application US/09726651A
 Patent No. 6448046
 GENERAL INFORMATION:
 APPLICANT: Donson, Jon
 APPLICANT: DAWSON, WILLIAM O.
 APPLICANT: GRANTHAM, GEORGE L.
 APPLICANT: TURPEN, THOMAS H.
 APPLICANT: TURPEN, ANN M.
 APPLICANT: GARGER, STEPHEN J.
 APPLICANT: GRILL, LAURENCE K.
 TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS
 FILE REFERENCE: 008010022CNUS01
 CURRENT APPLICATION NUMBER: US/09/726,651A
 CURRENT FILING DATE: 2002-05-02
 PRIOR APPLICATION NUMBER: US/08483,502
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: US 347,637

APPLICATION NUMBER: US 160,766
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160,771
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160,766
 FILING DATE: 05-MAY-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 363,138
 FILING DATE: 08-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 219,279
 FILING DATE: 15-JUL-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 18604-090574
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEFAX: 202-962-8300
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 289 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match 99.2%; Score 1420; DB 3; Length 289;
 Best Local Similarity 99.0%; Pred. No. 9.3e-138; Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Query 1 MIRFLVLSSLILTLTTPAVEGDSFRUSGATSSSYGVISNRKALPNERKUDIPLL 60
 Db 1 MIRFLVLSSLILTLTTPAVEGDSFRUSGATSSSYGVISNRKALPNERKUDIPLL 60

Query 61 RSSLPGSQRVALIHLTNAYDETSVAIDVINVYMGYRAGDTSYFNEASATEAKYVK 120
 Db 61 RSSLPGSQRVALIHLTNAYDETSVAIDVINVYMGYRAGDTSYFNEASATEAKYVK 120

Query 121 DAMKVTLPYSGNVERLQTAGKIRENTIPLGLPALSATIITLEFVNNSASAALMVLQS 180
 Db 121 DAMKVTLPYSGNVERLQTAGKIRENTIPLGLPALSATIITLEFVNNSASAALMVLQS 180

Query 181 TSEARYKPFEOQIGKRVDTKFLPLSALISLENSWALSALSQIQIQTASTNGQFEPVVLIN 240
 Db 181 TSEARYKPFEOQIGKRVDTKFLPLSALISLENSWALSALSQIQIQTASTNGQFEPVVLIN 240

Query 241 AQNQRTITNDAGVTSNIALLNRNNMAMDDDPVMTQSFGCGSYAI 289
 Db 241 AQNQRTITNDAGVTSNIALLNRNNMAMDDDPVMTQSFGCGSYAI 289

TELECOMMUNICATION INFORMATION
INFORMATION FOR SEQ ID: 17: 74;
TELEPHONE: (317) 337-4846
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
;
US-08-485-286-74

; ; GADB 0;
; ; LINYADET 82
; ; LINYADET 60
; ; BILQOTRAG 142
; ;
; ; US-C

TELEFAX: 312-679-9156
TELEX: 650 398-113B-6
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 247 amino acid
TYPE: amino acid
TOPLOGY: linear
MOLECULE TYPE: protein

Comprising Ribosome-Inactivating
Proteinase
ANSAASALMVLQIOTSBAARYKPIQOIQI
TNGQFESPVULINAQNQRVITNDAGI
TNGQFESPVULINAQNQRVITNDAGI
VAL 289
|:
YAI 267

alloy, Ltd.
t, 34th floor

S
0, Version #1.25
113B

336
691
430

BERLQHTAG 120
GKRVDKTF 202
GKRVDKTF 180
WVTNSIAL 262
WVTNSIAL 240
QY
Db
QY
Db
QY
Db
QY
Db
QY
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RESU
US C
; Se
; Pe
; Co
ating
Db
Db

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Query Match 84
Best Local Similarity 99
Matches 245; Conservativ
QY 24 DVSPRLSGATSSS
Db 1 DVSPRLSGATSSS
QY 84 SVADVTNTYIMGJ
Db 61 SVADVTNTYIMGJ
QY 144 IRENIPPGIPALDS
Db 121 IRENIPPGIPALDS
QY 204 PSLAIIISLNSWS
Db 181 PSLAIIISLNSWS
QY 264 LNRNNMA 270
Db 241 LNRNNMA 247

RESULT 10
US-08-477-484B-6
; Sequence 6, Application US
; General Information:
; Patent No. 5756599
; Application: Better, Marv
; Applicant: Carroll, St
; Applicant: Studnika, St
; Title of Invention: In
; Title of Invention: In
; Number of Sequences: 1
; Correspondence Address:
; Addressee: McAndrews
; Street: 500 West Mac
; City: Chicago
; State: Illinois
; Country: USA
; ZIP: 60661

; COMPUTER READABLE FORM
; MEDIUM TYPE: FLOPPY
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA
; APPLICATION NUMBER:
; FILING DATE: 07-JUN
; CLASSIFICATION: 530

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1.5%; Score 1209; DB 1; Length 247;
- 0.2%; Pred. No. 3.84-116; 0;
- Mismatches 2; Indels 0; Gaps 0;
- 0;
- GVFIISNLRKALPNERKLYDPLRLRSLPGQRYALHLNTYADETI 83
- TRAGDTSYFPEFEASATEAKVFKDMRKVYLPSGMYERIOTAAGK 143
- TRAGDTSYFPEFEASATEAKVFKDMRKVYLPSGMYERIOTAAGK 120
- VAITILFYNNANSASALMVLIQSIOSBAAKFKIEQIGKRDKTFL 203
- VAITILFYNNANSASALMVLIQSIOSBAAKFKIEQIGKRDKTFL 180
- LSKQIQAISTNGOESPVLINAONRVTINVDAGVNTIALL 263
- LSKQIQAISTNGOESPVLINAONRVTINVDAGVNTIALL 240
- 6/08477484B

C. D.
Stephen F.
Barry M.
immunotoxins Comprising Ribosome-Inactivating
proteins
69
3. Held & Malloy, Ltd.
Wilson Street, 34th floor

disk
-DOS/MS-DOS
Release #1.0, Version #1.25
PA:
US/05/477,484B
1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/425,336
 FILING DATE: 18-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 247 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 US-08-477-434B-6

Query Match 84.5%; Score 1209; DB 1; Length 247;
 Best Local Similarity 99.2%; Pred. No. 3.8e-16;
 Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 24 DVSFRLSGATSSSYGVFISNLKALPNERKLYDPLRSLSLPGSQRVALIHLTNYABTI 83
 1 DVSPRLSGATSSSYGVFISNLKALPNERKLYDPLRSLSLPGSQRVALIHLTNYABTI 60

Db 84 SVAIDVNTVNYIMGYRAGDTSYFNEASATEAKVVFKAQKTYLPIGSNGYERLQTAGK 143

Qy 61 SVAIDVNTVNYIMGYRAGDTSYFNEASATEAKVVFKAQKTYLPIGSNGYERLQTAGK 120

Db 144 IRENIPGLPGLPDAISAITLFLYNNANSAASALMVLQIOTSEARRYKFEQOIGKRVDTFL 203

Db 121 IRENIPGLPGLPDAISAITLFLYNNANSAASALMVLQIOTSEARRYKFEQOIGKRVDTFL 180

Qy 204 PSIAIISLENSWLSKQIQLIASTNNQFESPVLINANQRTITNDAGVTSNALL 263

Db 181 PSIAIISLENSWLSKQIQLIASTNNQFESPVLINANQRTITNDAGVTSNALL 240

Qy 264 LNRRNMA 270

Db 241 LNRRNMA 247

RESULT 11
 US-08-646-360-6

; Sequence 6, Application US/08646360
 ; Patent No. 537491
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnka, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; NUMBER OF SEQUENCES: 173
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA

ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 247 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 US-08-646-360-6

Query Match 84.5%; Score 1209; DB 2; Length 247;
 Best Local Similarity 99.2%; Pred. No. 3.8e-16;
 Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 24 DVSFRLSGATSSSYGVFISNLKALPNERKLYDPLRSLSLPGSQRVALIHLTNYABTI 83
 1 DVSPRLSGATSSSYGVFISNLKALPNERKLYDPLRSLSLPGSQRVALIHLTNYABTI 60

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Db 61 SVAIDVNTVNYIMGYRAGDTSYFNEASATEAKVVFKAQKTYLPIGSNGYERLQTAGK 120

Qy 144 IRENIPGLPGLPDAISAITLFLYNNANSAASALMVLQIOTSEARRYKFEQOIGKRVDTFL 203

Db 121 IRENIPGLPGLPDAISAITLFLYNNANSAASALMVLQIOTSEARRYKFEQOIGKRVDTFL 180

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Db 181 PSIAIISLENSWLSKQIQLIASTNNQFESPVLINANQRTITNDAGVTSNALL 240

Qy 264 LNRRNMA 270

Db 241 LNRRNMA 247

RESULT 12
 US-08-639-765-6

; Sequence 6, Application US/08839765
 ; Patent No. 6146631
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.

Db 61 SVAIDVNTVYIMGYRAGDTSYFNEASATEAKVFKDAMKVTLPYSGNYERLQTAGK 120 ;
 Qy 144 IRENIPGLPALSAITLFLYVYNSAASALMVLQDSEAAKYFEQOIGRVDKFL 203 ;
 Db 121 IRENIPGLPALSAITLFLYVYNSAASALMVLQDSEAAKYFEQOIGRVDKFL 180 ;
 Qy 204 PSAIISLENSWALSQIOIQAINTNGQFESPVULINAQNQRTITNDAGVTSNALL 263 ;
 Db 181 PSAIISLENSWALSQIOIQAINTNGQFESPVULINAQNQRTITNDAGVTSNALL 240 ;
 Qy 264 LNRNMA 270 ;
 Db 241 LNRNMA 247 ;
 RESULT 14 ;
 US-09-610-838-6 Application US/09510838 ;
 Sequence 6, Application US/09510838 ;
 Patent No. 6376217 ;
 GENERAL INFORMATION: ;
 APPLICANT: Better, Marc D. ;
 APPLICANT: Carroll, Stephen F. ;
 APPLICANT: Studnika, Gary M. ;
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating ;
 TITLE OF INVENTION: Proteins ;
 NUMBER OF SEQUENCES: 173 ;
 CORRESPONDENCE ADDRESS: ;
 ADDRESSEE: McAndress, Held & Malloy, Ltd. ;
 STREET: 500 West Madison Street, 34th floor ;
 CITY: Chicago ;
 STATE: Illinois ;
 COUNTRY: USA ;
 ZIP: 60661 ;
 COMPUTER READABLE FORM: ;
 MEDIUM TYPE: Floppy disk ;
 COMPUTER: IBM PC compatible ;
 OPERATING SYSTEM: PC-DOS/MS-DOS ;
 SOFTWARE: PatentIn Release #1.0, Version #1.25 ;
 CURRENT APPLICATION DATA: ;
 APPLICATION NUMBER: US/09/610,838 ;
 FILING DATE: 06-JUL-2000 ;
 CLASSIFICATION: ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US/09/136,389 ;
 FILING DATE: 18-AUG-1998 ;
 APPLICATION NUMBER: 08/646,360 ;
 FILING DATE: 13-MAY-1996 ;
 APPLICATION NUMBER: PCT/US94/05348 ;
 FILING DATE: 12-MAY-1994 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 08/064,691 ;
 FILING DATE: 12-MAY-1993 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 07/988,430 ;
 FILING DATE: 09-DEC-1992 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 07/901,707 ;
 FILING DATE: 19-JUN-1992 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 07/787,567 ;
 FILING DATE: 04-NOV-1991 ;
 ATTORNEY/AGENT INFORMATION: ;
 NAME: McNicholas, Janet M. ;
 REGISTRATION NUMBER: 32,918 ;
 REFERENCE/DOCKET NUMBER: 200-70.P4 ;
 TELECOMMUNICATION INFORMATION: ;
 TELEPHONE: 312/707-8889 ;
 TELEFAX: 312/707-9155 ;
 TELEX: 650 388-1248 ;
 INFORMATION FOR SEQ ID NO: 6 ;
 SEQUENCE CHARACTERISTICS: ;
 LENGTH: 247 amino acids ;
 TYPE: amino acid ;
 ;
 TOPLOGY: linear ;
 MOLECULE TYPE: protein ;
 US-09-610-838-6 ;
 Query Match 84.5%; Score 1209; DB 3; Length 247;
 Best Local Similarity 99.2%; Pred. No. 3; Be=112; Indels 0; Gaps 0;
 Matches 245; Conservative 0; Mismatches 0; ;
 24 DVSPRLSGATSSYGVFISNRLKALPERKLYDIPURSSLPSQSRALIHLTYADETI 83 ;
 Db 121 IRENIPGLPALSAITLFLYVYNSAASALMVLQDSEAAKYFEQOIGRVDKFL 180 ;
 Qy 204 PSAIISLENSWALSQIOIQAINTNGQFESPVULINAQNQRTITNDAGVTSNALL 263 ;
 Db 181 PSAIISLENSWALSQIOIQAINTNGQFESPVULINAQNQRTITNDAGVTSNALL 240 ;
 Qy 264 LNRNMA 270 ;
 Db 241 LNRNMA 247 ;
 RESULT 15 ;
 US-09-711-495-6 ;
 Sequence 6, Application US/09711485 ;
 Patent No. 6649742 ;
 GENERAL INFORMATION: ;
 APPLICANT: Better, Marc D. ;
 APPLICANT: Carroll, Stephen F. ;
 APPLICANT: Studnika, Gary M. ;
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating ;
 TITLE OF INVENTION: Proteins ;
 NUMBER OF SEQUENCES: 169 ;
 CORRESPONDENCE ADDRESS: ;
 ADDRESSEE: McAndress, Held & Malloy, Ltd. ;
 STREET: 500 West Madison Street, 34th floor ;
 CITY: Chicago ;
 STATE: Illinois ;
 COUNTRY: USA ;
 ZIP: 60661 ;
 COMPUTER READABLE FORM: ;
 MEDIUM TYPE: Floppy disk ;
 COMPUTER: IBM PC compatible ;
 OPERATING SYSTEM: PC-DOS/MS-DOS ;
 SOFTWARE: PatentIn Release #1.0, Version #1.25 ;
 CURRENT APPLICATION DATA: ;
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 FILING DATE: ;
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 APPLICATION NUMBER: 08/839,765 ;
 FILING DATE: ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 08/054,691 ;
 FILING DATE: 12-MAY-1993 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 07/988,430 ;
 FILING DATE: 09-DEC-1992 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 07/901,707 ;
 FILING DATE: 19-JUN-1992 ;
 PRIOR APPLICATION DATA: ;
 APPLICATION NUMBER: US 07/787,567 ;
 FILING DATE: 04-NOV-1991 ;
 ATTORNEY/AGENT INFORMATION: ;
 NAME: McNicholas, Janet M. ;

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; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-9189
; TELERX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-711-485-6

Query Match 84.5%; Score 1209; DB 4; Length 247;
Best Local Similarity 99.2%; Pred. No. 3 8e-116; Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 24 DYSFRUSGATSSSYGVFTSNLRLKALPWERKUDIPLRSUPGSQRVALIHLTNYADETI 83
Db 1 DVSFRLSGATSSSYGVFTSNLRLKALPWERKUDIPLRSUPGSQRVALIHLTNYADETI 60

Qy 84 SVAIDVNNVYMGYRAGDTSYFNEASATEAKYVFDAMRKTLPYSGNERTQAGK 143
Db 61 SVAIDVNNVYMGYRAGDTSYFNEASATEAKYVFDAMRKTLPYSGNERTQAGK 120

Qy 144 IRENIPGGLPALSATIILFYNNANSASALMLIGSTSEARYKTEQQIGRKVDTFL 203
Db 121 IRENIPGGLPALSATIILFYNNANSASALMLIGSTSEARYKTEQQIGRKVDTFL 180

Qy 204 PSAIAISLENSALSKQIOIATSTNNQFESPVVLINAQNQVITINVDAGVTSNALL 263
Db 181 PSAIAISLENSALSKQIOIATSTNNQFESPVVLINAQNQVITINVDAGVTSNALL 240

Qy 264 LNRNNMA 270
Db 241 LNRNNMA 247

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Search completed: April 12, 2005, 15:16:14
 Job time : 38.2034 secs